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RESULT RRYSHIT ID SHIP RRYSHIT 09-SEP-1994; 25-MAR-1994; /note-Misc-difference 289 mutant Poreine: acytylucosamine: 2 epimerase: N-acetylmannosamine: N-acetylneuraminic acid: renin-binding; enzymatic production: Porcine R79931 Standard: Protein: 402 AA W09526399-A1 Misc-difference Mise-difference Misc-difference 149 Sus scrota. 09-MAY-1996 (first entry) 24-MAR-1995; acylalucosamine-2-epimerase mutant 94JP-0216333. 94JP-0056271. 95WO-JP0U541 /note *18 /not.e-317 Location/Qualitiers /note-"wild type Ser substd. with Ard" "wild type Glu substil. with Glu' "wild type His substd. "wild type Asp substd. with Glu" with Tyr"

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Hest Local Similarity 34.8%; Pred. No. E
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(MARU) MARUKIN SHOYU KK

Maru I, Ohta Y. Isukada

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                                                                                                                                                                                                     Score 645; DB 16;
Pred. No. 1.3e-59;
                                                                                                                                                                                            Mismatches
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                                                                                                  page, and an iso-electric point of about 5. The amylase has optimum activity at about 55 degrees C and pH 9.5, and can be used in the production of improved detergents, e.g. laundry and hard surface cleaning detergent compositions. It is also useful in the production of sweeteners and ethanol from starch and also in the conventional starch-converting processes such as liquelaction and saccharilication. Alpha-amylase may
                                                                                                                                                                                              This is a Bacillus species alpha-amylase amino acid sequence. The alpha-amylase is derived from a strain of Bacillus, the preferred strain is Bacillus sp. NGIMB 40916. The mature protein sequence and the polynucleotide coding for the mature protein sequence are specifically claimed. The protein has a molecular weight of 55kb, as determined by she claimed. The protein has a molecular weight of 55kb, as determined by she
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y39296;
                      cardboard. The new alpha-amylase may also be used in modifying starch
the presence of alkaline fillers such as calcium carbonate, in the
textile industry for textile desizing, and in beer-making during the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ethanol; starch conversion; liquetaction; saccharification; pulp; paper; cardboard; liquocellulosic material; textile desizing; alkaline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y39296 standard; Protein; 532
                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                          Novel alpha-amylase enzymes derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09942567-AJ
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                                                                       pulp, paper and cardboard, from starch reinforced
                                                                                        also be used in the production of lignocellulosic materials, such as
                                                                                                                                                                                                                                                                                                                                                                                                         Outtrup H,
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/note- "the mature protein is specifically claimed"
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p0089, p0094, p0121 and p0128 libraries, respectively. It has 80.2% sequence identity to Sperobolus stapfianus sulphate penmease(ni 1907270). This sequence is used as a probe to isolate other plant sulphate
                                                               The present among and sequence is the corn sulphate permease, a sulphate assumitation protein. This sequence is from a contiq composed of clones cholo-pkou62.bio, ecolo-pkou7.lz], ecolo-pkou62.bi, phou64.cbie) 58r, p0089.csdch19r, p0094.csssq12r,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sulphate Permonse; sulphate assimilation protein; corn; contiq: probe; mapping; marker; plant breeding; chimeric gene; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corn sulphate permease 1.
                                                                                                                                             Claim 6; Page 49 41; 79pp; English
                                                                                                                                                                                  homotrogous
                                                                                                                                                                                            Nucleic acid tragments encoding sulfate assimilation proteins in plants and seeds useful as probes for isolating cDNAs and genes encoding
                                                                                                                                                                                                                                                N PSDB; 250481
                                                                                                                                                                                                                                                                                             Allen SM, Falco SC,
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                                                p0121.c1mmx00r and p0128.cpicz09r from cbn10, ccoln, cscle, p0004,
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hos 65; Conservative
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and as markers of traits linked to the denot like is useful for plant
breeding and to construct chimeric genes, used to create transpenie
plants with altered levels of sulphate permease. The sulphate permease
                           New Streptococcal protein, useful as a vaccine, for diagnosts of
                                                                                            Gilbert CEG.
                                                                                                                                                                                                                                                                   W0200006737 A2
                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae; vaccine; screening; protein antique; antibacterial; antiinflammatory; meningitis; infection; diagno
                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae type 4 protein sequence #17
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62: Conservative
                                                                                                                          MICKOBIAL TECHNICS LID
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                                                                                           Hansbro FM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.4%; Score 94; DB 2
19.1%; Pred. No. 0.53;
vative 46; Mismatches
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prominenced diseases and for screening agents capable of antagonizing or inhibiting expression of the protein

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Rest Local Similarity
Matches 72; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of anlagonising, inhibiting or interlexing with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. A05591 to A05614 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequences have antibacterial and antiinflammatory properties.

The profein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in
                                                                                                                                                                                                                                          02-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic assays. The proteins and nucleotides can be useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y81501 to Y81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. A05407 to A05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae.
                                                   Misc-difference
                                                                                                                                                                                                   Streptococcus pneumoniae SP0048 protein.
                                                                                                                                                                                                                                                                                                               W55100 standard:
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                                                                                                           Streptococcus
                                                                                                                                              detection; pneumonia; otitis
                                                                                                                                                             Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 74; 108pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GEW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGLMREAVTFTGEFVDSFEGR----LLNPGHGIEAMWFMMDIAQRSGDR------QLQEQ 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dkqatyyldqdqkmkrn-----awvqtsyv---qatqakviedwyyds------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGNWYFALDQEGKPLRQPYNVESDCFAAMAFSQYALASGAQEAKATALQAYNNVLRRQHN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vfdt-----hyqsw----fyikadanyaenewl---kqqddyfylksqgymaksewve
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                                                                                                                                                                                                                                      (lirst entry)
                                                                                                           pneumoniae
                 /note- "encoded by ARK"
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              FGYLNRRGEV 360
                                                                                                                                                                                                                                                                                                                 Protein; 368
                                    /label- unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----qikgkdyyfksggylltsqwinqayvnasgakvqqgwlfdkqyq 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.38; Score 92.5; DB
                                                                                                                                                media; meningitis
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E X X A X X I D

24-MAY-2000 (first entry)

Streptococcus pneumoniae protein sequence ID204 · 4117.1.

RESULT 9 Y81667

Y81667 standard; Protein; 678

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        В
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibodies in standard immunoassays, especially for diagnosing of monitoring infections. Antibodies which bind the protein are used to detect corresponding antiquens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 c.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, offils media or meningitis. Probes based on the public acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The nucleic acid sequence encoding the Streptococcus pneumoniae The nucleic acid sequence encoding the Streptococcus pneumoniae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 65; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; V27361
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353 tsidayrvndhaew
                                                                            364 LK------GGKW
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                                                                                                                                                                                                                             304 LWWVHLETLVALAKGHQATGQEKCWQWFERVHDYAWSHFADPEYGEWFGYLNRRGEVLLN 363
                                                                                                                                                 sswyyl-----nsngsmkvngwfg------vggkwy-yvntsgelavn
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                                                                                                                                                                                                                                                                                                                                                                                      AMWEMMDIAQRSGDRQLQEQAIAVVLNTLEYAWDEEFGGIFYFIDRQGHPPQQLEWDQ-K-30-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 AA;
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19.7%; Pred. No. 0.26;
        366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matchess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection and diagnosis of S. pueumoniae. The protein sequences are also useful for screening an agent capable of antagonisting, inhibiting or interfering with the function of expression of the proteins in which the area is useful for freatment or prophylaxis of S. pueumoniae intection and meningities. A0559 to A05644 represent primers used to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated from Streptococcus pneumonide. A05407 to A05590 represent specifically claimed nucleotide sequences isolated from S. pneumonide. The sequences haze antibacterial and antibullammatory properties. The protein sequences, and fragments of them, are useful as immunodens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chaim 6; Page 89; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the present inzention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 101. 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae; vaccine; screening; protein antiqen; antibacterial; antirullammatory; meningitis; intection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic assays, the proteins and nucleotides can be useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YBISUL to YBISUS represent specifically claimed protein sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPT: 2000 195300/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MICK ) MICKOBIAL IECHNICS LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and/or antiques, the nucleotide sequences can be used in vaccines and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEA OF
                                                                                                                                                                                                                                                     274 ydshoqawyytksqqymtanewiwdkeswtylksdqkiaekewvydshsqawyytksqqy
                                                                                                                     250 ATAVVINILEYAWDEEF GGTEYELLARGGH PPQGLEWDQKIW
                                                                                                                                                                                                                                                                                    156 PROOYEKSYINTERELKSI.AVEMILAN LELEMEMELLEPTTVEEVLAGIVREVMIDELDPE 214
                                                                                                                                                                                                                                                                                                                              lll dkaatyyldadakmkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 VESTIMEONROVWOFAVEYNREE PRPOMEETARROAD
                                                                                                                                                                                                                                                                                                                                                                    56 DENWYFALDOEEKFIROPYNVESDCFAAMAFSOYALASOAQEAKATALOAYNNVIRROHN 155
                                                                             swlyikenanya dkewitenahyyylksaaymaanewiwdkeswtylktdakmaekewv
                                                                                                                                                                                                      TOTAMERAALBIGEEADSEEGK - ATTNBGROTEVAMMENTVÖRSOOK
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                                           HILETICVALAKOHÇA TÖÇEKEM
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990[S 0125164
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                                                                                                                                                                                                                                                                                                                                                                                                             hydsw
                                                                                                                                                             qikqkdyytksqqylltsqwinqayvnasqakvqqqwltdkqyq 214
                                                                                                                                                                                                                                                                                                                                                                                                         tyikadanyaenewl - kqaddytyiksqqymaksewve 110
                                                                                                                                                                                                                                                yikadqqhaekewl - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Mismatches 109; Indels 159; Gaps
                                                                                                                                                                                                                                                                                                                            awvqtsyv:- qatqakviedwvyds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 678;
                                         OWFERVHDYAWSHFADDEY 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FLARIGRDQ 95
                                                                                                                                                                                                      QLQEQ 264
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29-MAR-1995;
29 SEP 1995;
                                                                                                                               dependency. The variants can also have increased alpha amylolyric activity (especially at pH values in tende of 85 10.5), and improved binding of a particular substrate. These variant alpha amylases also possess improved specificity to a particular substrate, and/or improved
                                                                                                                                                                                                            thermal stability (such as at temperatures in the range of 40-70 degree Celeius), and/or oxidation stability, and/or reduced calcium ion
                                                                                                                                                                                                                                                                                         nortagenesis of the DNA sequences encoding the parent alpha amylases represented by W12955, W12956, R81835 and R81836. W12137 W12140, and
                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha amylase variants - with improved thermal and exhdation stability and reduced calcium ion dependency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPT: 1996 471424/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha amylase: determent: thermal stability; oxidation stability; enzymes calcium (on dependency; alpha amylolyt)e activity; washing composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha amylase variant delta182 + delta184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W1214 standard; protein; 483 AA
Sequence
                                                  the alpha amylase variants can also be used in papermaking and beer making processes. These variants can also be used in the production
                                                                                           specificity with respect to cleavage of substrate. These sequences can be used in determent and washing compositions, and for textile designing
                                                                                                                                                                                                                                                                      W12143 are specifically variants of the alkaphilic Bacillus strain NCIB
                                                                                                                                                                                                                                                                                                                                 variants of the
                                                                                                                                                                                                                                                                                                                                                 W12098-W12144 represent alpha amylase variants of the invention
                                                                                                                                                                                                                                                                                                                                                                                          Example 3; ; lllpp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bisward frantzen H. Borchert I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Nevo ) Nove Nertelsk As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05 FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08 - AUG - 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09623873-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W12144;
                                    of sweeteners and ethanol from starch.
                                                                                                                                                                                                                                                  12513 alpha-amylase shown in R81836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 mtanewiwdkeswtylksdyki 355
  4H AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (tirst entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95DK 0000126
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                                                                                                                                                                                                                                                                                                                             invention were created using site directed, or random,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGATMENGEA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Svendsen
                                                                                                                                                                                                                                                These variants can have improved
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Query Match
Rest Local Similarity
Matches 87; Conserv

Conservative

4.1%; 19.8%;

Pred. No. 1;

DB 17; Length 484;

126 nrngeisady

4 HEROFIAQQYYQALHQDVI.PFWEKYSI.DRQGGGYFTGI.DRKGQVFDIDKFTWI.QNRQVWQ 6-3

46; Mismatches 124; Indels 182;

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                 TTTX
                                                                                                                                                                                                                                              = X = X = X = X = X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hovine lysosomal alpha-mannosidase (LAMAN) R221H mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1998 (first entry)
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(NILSZ) NILSSEN O.
                                                                                                           (BERG/) BERG I.
                                                                                                                                                                                                                                        15-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                   15-JAN-1447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 - JUL - 1997.
                                                           (HEAL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 myvqqukadqvwhditqnk 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 EEVLAGIVREVMIDELDREIGLMREAVIRIGEEVDSEEGRILNRGHGIEAM---WEMMDI 252
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                                                     HEALY P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation causing bam in Angus and related breeds of cattle has also been identified. PCR primers (see T91088 99) are provided for use in a claimed method for detecting these mutations. Compared with known enzymatic methods, smaller samples are needed, LNA is stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosis and screening for bovine alpha mannosidosis: by detect mutation(s) in alpha-mannosidase gene, also nucleic acid encoding the enzyme and derived oligonucleotide primers
27-MAR-1998 (first entry)
                                          W26683;
                                                                              W26683 standard; Protein; 999 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quicker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2: Page -; 85pp; English.
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(BERGZ) BERG L.

(BERGZ) BERG L.

(TOLLZ) TOLLEBRATIO OK.
                                                                             comparises detecting the presence of absence of bam causing mutations in the LAMAN gene; another point mutation causing bam in Galloway earlie has also been identified. Priv primers (see T94000-8-93) are provided for use in a claimed method for detecting these mutations. Compared with known enzymatic methods, smaller samples are needed, DNA is stable during transport and storage, and the test is more
                                                                                                                                                                                          This dycosylated polypeptide comprises a mutant bovine lysosomal alpha mannosidase (LAMAN) that causes borine alpha mannosidosis bam) in Andus and related breeds of cattle. The F42H mutation
                                                                                                                                                                                                                                                                              bioquosis and screening for boyine alpha mannosidosis - by detecting mutalion(s) in alpha mannosidase gene, also nucleic acid encoding the enzyme and derived oligonucleotide primers
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                                                                                                                                                                                results from a point mutation of the LAMAN coding sequence (see
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                                      are duced by adaptation of the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JAN 1997:
                                                   the sequence for the £3211 mutant alpha mannosidase was
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Query Match 4.1%: Score 87.5; Di-Best Local Simularity 17.5%; Pred. No. 4.6;

Matches

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Mismatches

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23-DEC-1993;
                                                                       Alpha sub unit polypoptide of human beta 2 integrin—used to identity potential antiinflammatory agents, for the treatment graft arteriosclerosis, inflammatory bowel disease, asthma, et
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Mise-difference 1128
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Hest Local Similarity 20.2%; Prod. No. 4.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library. Alpha d is involved in cell migration, phagocytosis and cell-cell interaction. Recombinant alpha d polypeptides can be expressed in transformed host cells for use in assays for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybridoma 199M and antibody secreted by it—specific for new
beta2 integrin subunit, useful to detect subunit in cells and
modulate its activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This polypeptide comprises the rat homologue of a novel homan beta 2 integrin subunit, designated alpha d (see W23049). Its sequence was deduced from a cDNA clone (see T79257) isolated from a spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 17; Page 170–175; 222pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyright (c) 1993 - 2000 Compugen Etd.
/cyii2_5/ptodata/2/lad/5A_COMB.pep:*
/cyii2_5/ptodata/2/lad/5B_COMB.pep:*
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/cyii2_5/ptodata/2/lad/pcTUS.COMB.pep:*
/cyii2_5/ptodata/2/lad/hackiiles1.pep:*
                                                                                                                                                                                                                                                                                                              164575
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Fred. No. is the number of results predicted by chance to have a score dreater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Алена				
. N	Score	Mat ch	Match Length	E	10	Description
_	554	12.5	402	-	US-08-554 704A-4	Sequence 4, Appli
7	694	4.4	402	κ.	US-09-006-021-4	<u>.</u>
ند	591	32.2	402	_	IJS-ÿ8-55∢-7∪3A-]	
٠	691	42.2	402	N	US-09-006-021-1	_
Jī	668	<u> </u>	419	_	-08	i.
5	899	31.1	419	N	US-09-006-021-3	ښ
7	645	30.0	417	_	US-08-553-703A-2	2,
သ	645	¥0.0	417	N	-09	ν,
٠.	87.5	4.1	1161		US-08-485-618-55	
1 0	87.5	4.	1161	_	-08	5
1.1	87.5	4.1	1161	ν	US-08-605-672-55	55,
L	87.5	4.1	1161	~	US-08-482-294A-55	55.
	87.5	4.1	1161	ĸ	US-08-944-464-55	G G
14	85	4.0	4 H 5	2	US-08-446-803-2	N
	α F	4. U	485	~	80-	2
16	86	4 . C	485	u.	US-08-600-656-2	Ν,
17	84.5	₹.9	729	_	US-08-070-165F 6	<u>_</u>
٦ ۲	84.5	3.9	7.29	۷	ปร-08-8ห5-418-6	j.
14	84.5	3.9	7 1 1		US-08-070-165F-10	10,
20	84.S	4.4	7 + 1	2	US-08-885-418-10	10,
2]	<u>~</u>	÷.⊗	357	N	US-08-475-254-11	
22	Ξ	œ	354	S	5474933-8	
23	74.5	3.7	1155		US-08-286-889-46	Sequence 46, Appl
24	79.5	3.7	1155	_	US-08-485-618-46	46,
2.5	79.5	3.7	1155	_	US-08-362-652-46	46,
27	79.5	3.7	1155	N	US-08-605-672-46	46
27	74.5	₹.7	1155	Ν	US-08-482-293A-46	46,
28	74.5	4.7	1155	٨	US-08-943-363-46	46,

Sequence 1, Appli	1 US-08-019-870-1	773	3.6	76.5	Sil
Sequence 10	4 PCT-0895 04258-10	129	3.6	77.5	4
Sequence 1:	3 US-08-722 126A-10	124	3.6	77.5	٠
Sequence 4.	1 US-08-385-470-4	616	يد ج	78	4 2
Sequence 2.	1 05-08-385-370-2	616	3.6	78	_
Sequence 37.	2 US-08-943 464-47	1311	3.7	78.5	‡
. Actionbas	2 US :08 - 482 - 293A 37	1151	3.7	78.5	£
Stoffenor	2 08-605-672-37	1151	4.7	78.5	æ
Sequence 42	1 US-08-362-652-37	1151	4.7	78.5	. 7
Sequence 37	1 US 08-485-618-37	1151	3.7	78.5	3.6
Sequence 37	1 08-08-286-889-37	1.15.1	3.7	7H.5	ா
6.2 acinombos	2 US 08 - 557 - 122A - 29	504	3.7	7×.5	مت
Sequence 54	2 08-08 943-363-53	1161	4.7	79.5	
re contambase	2 US-08-482-253A-53	1151	3.7	79.5	^
r, activities	2 08-08-605-672-53	1161	3.7	74.5	-
Sequence 64	46.2-65	1161	4.7	74.5	Ξ
Sequence 53	1 US 08 485-518-53	1161	4.7	74.5	ئي

ALIGNMENTS

; Sequence 4, Application US/U8553703A ; Patent No. 5795767

GENERAL INFORMATION:

RESULT 1 US-08-554-703A-4

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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-553-703A-4
                                                                                                                                                          INFORMATION FOR SEC 10 NO: 4:
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APPLICANT: 04HA, YASUHIRO
APPLICANI: ISKKADA, YOJ
TILLE OF INVENTION: EFTMERASE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             TELEPHONE: 714-760-0404
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER:
                                                                          LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                   NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 30-NOV-CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: 18M Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 620 Newport
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHUNTRY:
                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
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Overy Match 32.3%; Score 694; TB-1; Lenath 402; Hest Local Similarity 34.8%; Pred. No. 7.4e-65; Matches 143; Conservative 77; Mismatches 153; Indels

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; Mephence 4, Application US/09006021
; Patent No. 5994105
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                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SECTIONS:
                                                                                                                                                                                                                                                                           SECURIOR CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MARH, ISAEHMI
APPLICANT: OHIA, YASHHIRO
APPLICANT: TSUKADA, YOJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARF: FASTSEQ Version 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESTONISTNOTE ALBERTSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 714 760 0404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRIDE APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRIS MMILLO LA DESCRIPTION DE LA MINIMA ERISTE DE LA MINIMA EN LA MINIMA ENTLA MINI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERALLNE SYSTEM:
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: Abor'Toded.
                                                                                                                                                                                                    LENGIH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 714 760 9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEGISTRALION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILLY: DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/006, 021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Knobbe, Martens, olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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                                                                      STRANDEUNESS:
                                                                                                                                                                                                                                                                                                                                                                                                         I FILEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92660
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J. Banifel E
TORR: 44,115
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30 NoV 1995
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TELEPHONE: 714 760-0404
                                                                                                                                                                                                                                                APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MARU, ISAFUMI
APPLICANI: OHIA, YASUHIRO
APPLICANI: ISUKADA, YOJI
                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                          ALIGENEY/AGENT INFORMATION:
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                                                              NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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                                              REFERENCE/DESKILL NUMBER:
                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                        COMPUTER:
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                                                                                                                                                        APPLICATION NUMBER
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34.8%; Pred. No. 7.4e 65
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: Patent No. 5994105
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Molecule Type: poptide
EKAGMENT Type: N-terminal
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson
SIREEL: 620 Newport Center Drive
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANI: MARU, ISAFUMI
APPLICANI: OHIA, YASUHIRO
APPLICANI: TSUKADA, YOJI
                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/006,021
                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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TELEX:
                                                                                                     SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                MEDIUM TYPE:
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CLASSIFICATION:
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                                                                                                                      OPERATING SYSTEM:
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349 OFRDPEYGEWEGYLNREGKVALLIKGGPFKGCFHVPRCLAMCHEMLSALLS 399
                                          341 HFADPEYGEWFGYLNRRGEVILNIKGGKWKGCFHVPRALWICAETLQLFVS 391
                                                                                         289 HGGLEYFQDADGLCPTQLEWAMKLWWPHSEAMIAFLMGYSESGDFALLRLFYQVAEYIFR
                                                                                                                                     281 FGGTFYFIDRÖGHPPGGLEWDGKLWWVHLEILVALAKGBGAIGGEKCWGWFERVHDYAWS
                                                                                                                                                                                                                                   222 VTPTGEFVDSFEGRLLNPGHGIEAMWFMMDIAQRSGDRQLQEQAI-AVVLNTLEYAWDEE
                                                                                                                                                                                                                                                                                  183 MMLLCLVEQLGEEDEBLAGRYAQLGHW----CARRILGHVQRDGQA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Altman, Daniel E
REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 WMYCRLYKKLERFHRPELLDAAKAGGEFLLRHARVAPPEKKCAFVLTRIGIKPVKVQKSIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 714-760-04
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 WOFAVEYNRLE--PKPQWLEIARHGADFLARHGR--DQDGNWYFALDQEGKPLKQEYNVF ]]]/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I HILHX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 RROELAGOYYOALHOD- -VLPFWEKYSLDROGGGYFIGLDRKGGVFDIDKFIWLGNRGV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KERETLQAWKERVGQELDRYMAFWLEHSHDREHGGPFICLGRDGRYYDDLKYVWLQGRQV 62
                                                                                                                                                                                         VSEDGEELSGCLGRHQNPGHALEAGWELLRHSSRSGDAKLRAHVIDTFLLLPFRSGWDAL
                                                                                                                                                                                                                                                                                                                                      MILANLILEM
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45.0%; Pred. No. 1.56-64;
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                                                                                                                                                                                                                                                                                                                                 -----EWILPPTTVEEVIAQTVREVMTDF1DPEIGLMREA 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74; Mismatches 155;
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RESULT 5
US-08-553-703A-3
US-08-553-703A-3
Patent No. 5795767
GENERAL INFORMATION:
APPLICANT: MARD, ISABUMI
APPLICANT: TSUKADA, YOJI
111LE OF INFOLION: EPIMERASE
NUMBER OF SEQUENCES: 9
COKRESPONDENCE ADDRESS: 9
COKRESPONDENCE ADDRESS: STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
SIATE: CA
COUNTRY: U.S.A.
ZIP: 92660.S
ZIP: 92660.S
MEDIUM TYPE: Diskette
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Stephene 4. Application US/09006021
Usfort No. 5991105
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Best Local Similarity (5.6%) Pred. No. 4.3c-62;
Matches 145; Conservative 71; Mismatches 151; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Querry Match
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                                               APECITANT: MARU, ISAFUMI
APECITANT: OBEA, YASHBILEO
APECITANT: ISHKADA, YOL
APECITANT: ISHKADA, YOL
APECITANT: ABROMENOES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: poptide ERACMENT TYPE: N terminal
CORRESPONDENCE ADDRESS
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TELEPHONE: 714 /60 0404
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REGISTRATION NUMBER: 34,115
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                                                                                                                                                                              OPERALING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 31.1%; Score 668; DH 2; Length 419; Hest Local Similarity 35.6%; Pred. No. 4.3e 62; Matches 145; Conservative 71; Mismatches 151; Indels 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Tinear
MOLECULE TYPE: poptide
FRAGMENT TYPE: N (erminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPERENCE/DOCKET NUMBER: TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISITES:
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EKTOR APPLICATION DATA:
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APPLICATION NUMBER: US/09/006,021
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                                                                                                                                                                                      228 NVSEDGKELEGTAARHONEGHILGAGWELLQYALKKGDEKLQKHILDKELLLEFHSGWOF 287
                                                                                                                                                                                                                                  221 AVIPIGEEVESTEGRILNEGHGIEAMWEMMOIAQRSGDRQLQEQAI AVVLNTILEYAWDE 279
                                                                                                                                                                                                                                                                                      I 8 - MMI.I.NI. · ·
                                                                                                                                                                                                                                                                                                                             177 MILANLILEMENTLAPTIVEEVLAQIVKEVMIDELDPEIG
                                                                                                                                                                                                                                                                                                                                                                              123 SECTYTMAMNELWKYTGEMHYGREAVEMMDGITHWVKEDFAGLGREGLSGITATEFMAVE 182
                                                                                                                                                                                                                                                                                                                                                                                                                             118 SIMTEAAMAESQYALASGAQEAKATALQAYNNVLK KQHNPKQQYEKSYFGTKFLKSLAVP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe, Martens, clson
SIRFEL: 520 Newport Center Brive
CLIY: Newport Beach
SIAIE: CA
                                            340 SHEADPEYGEWEGYLNERGEVILLNIKGGKWKGCEHVPRALWIGAETI 385
                                                                                           ZBS EHGGLEYEQDADDLCYTQLEWNMKLWWPHTEAMTAFLMGYROSGDFALLNLFYJVAEYTE <4/
                                                                                                                                       280 EFGGTEYFIDROGHIPPOOLEWDOKLWWVHLEILVALAKGHQAIGQEKGWOWFEKVHDYAW 339
348 BOFKDPEYGEWFGYLNOEGKVALIIKGGPFKGCFHVPRCLAMCEOII 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 WMYC'RLYKTEEKERKVELLDAAKAGGEFILSYAKVAPPGKKCAFVLTQDGKEVKVQRTTF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: Sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFIWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERALING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2 MQEAVEYNRLE: PKPQWLETARBGADELARBGR:--DQDGNWYFALDQEGKFLRQFYNVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * KERETLOVMKORVOGELDSV LAEMMEHSHOGERGEF FOLGRUBOVVDHLKYVMLOGROV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KRQELAQQYYQALHQD----VLPEWEKYSLDRQGGGYFTGTLDRKGQVFDTDKFTWLQNRQV-61
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IBM Compatible
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                                                                                                                                                                                                                                                                                 ---- VEQLGEED--EEMILIKY AELGDWCAHRILQHVQKIRQQVVLE 227
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; Sequence 2, Application US/08554704A

RESULT

7:80-58-5039-50

SENERAL INFORMATION:
APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, VASUHIRO
APPLICANT: TSUKADA, VOJI

TITLE OF INVENTION: EPIMERASE NUMBER OF SEQUENCES: 9

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349 EWFGYLNERGEVLLNLKGGKWKGCFHVFRALWLCAETL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
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APPLICATION NUMBER: US,
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NAME: Altman, Daniel E
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                                                                                    2 47
297 DADNECPTOLEWAMKLWWPHSEAMIAFLMGYSDSGDPVLLRLFYOVAEYTERQTRDPEYG 356
                                         289 DROGHPPOOLEWDOKLWWVHLETLVALAKGHOATGOEKCWOWFERVHDYAWSHFADDEYG 348
                                                                                                                                                                         183 MMILNI.VEQL-----GEADEELAGKYAELGDWCARRILQHVQRDGQAVLENVSEGGKEL 236
                                                                                                                                                                                                                       177
                                                                                                                                                                                                                                                              123 SECFYTMAMNELWRATGEVRYQTEAVEMMDQIVHWVQEDASGLGRPQLQGAPAAEPMAVP 182
                                                                                                                                                                                                                                                                                                            118 SINYHAAMAESOYALASGAOBAKATALQAYNNVLR-ROHNPKGOYEKSYPGTRPLKSLAVP 176
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SOFTWARE: FastSEQ Version 1.5
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CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                       64 WMYCRLYRTTERFRHAQLLDAAKAGGEFLLRYARVAPPGKKCAFVLTRDGRFVKVQRT1F 122
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REGISTRALION NUMBER: 34,115
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                                                                                                                                                                                                                                                                                                                                                                                            62 WOFAVFYNKLE: PKPQWLEIARHGADFLARHGR--LØDGNWYFALDØEGKPLKØPYNVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : YSc/Tender1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 RRQELAQQYYQALHQD---VLPFWEKYSLDRQGGGYFTCLDRKGQVFDTDKFIWLQNRQV 61
                                                                                    PGCLGROQNPGHTLEAGWELLRHCIRKGDPELRAHVIDKELLLPFHSGWDPDHGGLFYFQ 296
                                                                                                                              DSFEGRII.NPGHGIEAMWFMMDIAQRSGDRQLQEQAI-AVVLNTLEYAWDEEFGGIFYFL 288
                                                                                                                                                                                                                  MILANLTLEMEWLLPPTTVEEVLAQTVREV-----MTDFLDPEIGLMREAVTPTGEFV 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.0%; Score 645; DB 1; Longth 417; 34.7%; Pred. No. 1.1e-59;
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                                                                                                                                                                                                                                                                                                                                                    Query Match (0.0%; Score 645; DR 2; Length 417; Best Local Similarity (4.7%; Pred. No. 1.1+ 53; Matches 138; Conservative 75; Mismatches 164; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MARU, ISAFUMI
APPLICANT: OHIA, YASUHIRO
APPLICANT: TSUKADA, YOJI
TIILE OF INVENTION: EPIMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DAIE: 30-NOV-1995
ALLORNEY/AGENI INFORMATION:
NAME: Altman, Daniel E
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Fast SEC Version 1.5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SECUENCES:
  183 MMLLNLVEQL----
                                    177 MILANLILEMENLLIPTITVEEVLAQTVREV----- MIDFLDPETGLMREAVIPTGEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Altman, Daniel E
REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/5 FILING DATE: 30-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERALING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
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                                                                                                                                                                          63 WMYCRLYRIFERFRHAULLDAAKAGGEFILRYARVAPPGKKCAFVLIRDGRPVKVQRITF 122
                                                                                                                                                                                                                   62 WQFAVFYNRLE--PKPQWLEIARHGADFLARHGR--DQDGNWYFALDQEGKFLRQPYNVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                    3 KERETLQAWKERVGQELDRVVAFWMEHSHDQEHGGFFTCLGKEGRVYDLLKYVWLQGRQV 62
                                                                                     SECFYTMAMNELWRATGEVRYQTEAVEMMUQIVHWVQEDASGLGRPQLQGAPAAEFMAVF 182
                                                                                                                              SDCFAAMAFSQYALASGAQEAKAIALQAYNNVLR-RQHNPKGQYEKSYPGTRPLKSLAVP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92660
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                                                                                                                                                                                                                                                                           US OB 485 618 55
                                                                                                                       4.1%; Score 87.5; DR 1; Length 1161;
Bost Local Similarity 20.2%; Prod. No. 2.8;
Matthes 79; Conservative 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 55. Application US/08485618
Fatent No. 5728533
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APPLICANT: Van der Vieren, Monica
APPLICANT: Vallon: No. 572853 kel Buman / Integrin Alpha Subunit
NUMBER of ENVISION: No. 572853 kel Buman / Integrin Alpha Subunit
NUMBER of Skytteness: 103
Coddessendence Alphaess:
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APPLICATION NUMBER: US 08/362,652
FILING DATE: 21 DEC 1994
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APPLICATION NUMBER: US 08/1/3/49/
FILING DATE: 23 DEC 1993
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APPLICATION NUMBER: US |
FILING DATE: 5 AUG 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
       161 EKSYPCIEPLKSLAVPMILANLILEMEWILLPP
                                                    155 FILIDGSGSTNORDFAQMKD:
                                                                                                 101 FALFOEGKELROPYNVESDCEAAMAFSQYALASGAOEAKATALOAYNNVLRROHNPKGQY 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 DADNECPTOLEWAMKLWWPHSEAMTAFLMCYSDSCDPVLLRLEYQVABYTERQFRDPEYC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 DROCHEPOOLEMOKIMMVHILETIVALAKGHOATGOEKCMOMFERVHDYAMSHFADREYG 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPULER: IBM PC COMPATIBLE
OPERALING SYSTEM: PC-100S/MS DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 48,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 4.65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 48,659
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                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                  1161 amino acids
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233 South Wacker Drive, 6300 Sear Tower
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312 474 9448
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                                                                                                                                                49) Mismatches 123; Indels 141; Gaps
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Patent No. 5766850
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MOLECULE FYPE: protein
                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gallatin, w. Michaec.
APPLICANT: Van der Vieren, Monica
IIIIE of INVENTION: No. 5766850el Human 2 Integrin Alpha Subanit
                                                                                     SEQUENCE CHARACIERISTICS:
LENGTH: 1161 amino aci
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ANTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Josep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Ploppy disk
COMPHER: IBM PC compatible
OPERATING SYSTEM: PC-1882MS DOS
SCHTWARE: Futentli Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 TIDBOKYKDPLEYSDVTPAADKAGTIRYATGV6DAFQEFTALKELNI16SAFPODHVFKV - (17
                                          TYPE: amino acid
topology: linear
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 38,659
                                                                                                                                                                                                                                                                          NAME: Williams Jr., Joseph A. REGISTRAFION NUMBER: 38,659
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CHIY: Chicago
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/286,889
FILING DATE: 5:AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                               TELEPHONE: $12,474+6300
TELEFAX: $12-474+0448
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: Patent No. 5817515
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GENERAL INFORMATION:
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                                                                                                                      APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION UNAIA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFIMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANI: Van der Vieren, Monica
TILLE OF INVENTION: NO. 5817515el Human
NUMBER OF SEQUENCES: 103
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                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                        FILING DATE: 23-DEC-1993 PRIOR APPLICATION DATA:
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                                                          NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659 REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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STAIE: Illinoi
TELEPHONE:
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Mismatches 123; Indels 141; Gaps
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US-08-482-293A-55; Sequence 55, Applic; Patent No. 5831029
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Matches 79; Conserv
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INFORMATION FOR SEQ 10 NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
        APPLIANTE

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: US 08/173,497

APPLICATION NUMBER: 23-DEC-1993
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                                                                                                                                                                     CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
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                                                                                                                                             APPLICATION NUMBER:
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APPLICATION NUMBER:
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US 08/286,889
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                                                                                                                                                                                                                                                                                                                                                 US 08-943 363 55
                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                       Sequence 55, Application US/08943363
Patent No. 5837478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mait others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.1%; Score 87.5; Direct Local Similarity 20.2%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NOT 55:
                                     COMPUTER READABLE FORM:
                                                                                                                                                          CORRESSOR: Marshall, o'toole, Gerstein, Murray & Worum
                                                                                                                                                                                                  APPLICANT: Callatin, W. Michael
APPLICANT: Van der Vieren, Monica
IIIIE of INVENTION: No. 58/04/801 Human / Lintegrin Alpha Subunit
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER:
APPLICATION NATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                 COUNTRY:
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Topology: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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    COMPUTER:
                       MEDIUM TYPE:
                                                                                                      : H1V1.5
                                                                                                                                            STREET
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                                                                                 United States
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t: Floppy disk
IBM be compatible
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US 08-446-803-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                              48a GAPHYYECIKOOOVSVEPVPGVKGKWOTEAIL 511
                                                                                                                                                                                                                     426 PRHOHIGKVVIFTOEARHWRPK----- SEVROTQIGSYFGASICSVDVDROGSXDLVI.1 479
                                                                                                                                                                                                                                                                    319 --HOATGO----EKCWOWEERVHDYAWSHEADDEYGEWEGY------INRRGEVILLNIK 365
                                                                                                                                                                                                                                                                                                                         375 SWS - GGAFLY- ---PPNTRPTFINMSQENVDMRDSYLGYSTAVAFWKGVHSIILGA 425
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112 474-0448
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REFERENCE/INCKET NUMBER: 27866/42684
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; Sequence 2, Application US/08446803; Patent No. 5824531

GENERAL INFORMATION:

APPLICANT: APPLICANT:

ottrup, Helle Bisgard-Frantzen, ostergaard, Peter

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-08-446-803-2
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INFORMATION FOR SEQ ID NO: 2:
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REGISTRATION NUMBER: 38,711
REFERENCE/DECKEL NUMBER: 4157,204-US
LELECOMMUNICATION INFORMATION:
LELECOMMUNICATION (NFORMATION)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUFTWARE: Fatentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,803
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MEDIUM TYPE: Ploppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Afforney/AGENT INFORMATION:
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APPLICANT: Van Det Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
NUMBER OF SEQUENCES: 5
443 GONKAGOVWHILLIGNK 458
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                                          455 -- NRRGEVLLNLKGGK 468
                                                                                                                                   $16 AKCHOATGOEKCWOWFERVHDY-----AWSH----
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SIKANDEDNESS: single
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	Patent N	Patent, No. 5856164
	APPLICANT:	INFORMATION: CANT: Ottrup, Helle
٠.	APPLI	CANI: Bisgard Frantzen, Henrik
	APPLI	CANT: Osteryaaid, Peter Rahbek CANT: Rasmussen, Michael Dolbeid
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** **	NUMBE	OF INVENTION: AIRCHING MACHING AMYLASO
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	S C L	Y: New York
٠. ٠	COII	NTRY: USA
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	MED	IUM TYPE: Floppy disk
	O X	COMPUTER: IBM PC compatible
	SOF 5	WARE: Patentin kelease #].0, Version #1.25
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	SELSE VTD	CLASSIFICATION: 435
٠.	APP	APPLICATION NUMBER: US 08/446,803
	ATTOR	NEY/AGENT INFORMATION:
٠. ٠.	REG	E: Harrington, James J. ISTRATION NUMBER: 38,711
• •	# E E	ERENCE/DOCKET NUMBER: 4157.204-US
	TRI	EPHONE: (212) 867-0123
	TEL INFORMA	TELEFAX: (212) 878-9655 INFORMATION FOR SEU ID NO: 2:
	SEQUE	NCE CHARACTERISTICS:
•••	d.k.1	E: amino acid
	: S = X	ANDEDNESS: single
<u> </u>	-198-80-5E MOLEC For	INPULATE: LIBERI MOLECULATIVE: peptide 1-861-847-9
	Query Ma Best Loc Matches	Ouery Match 4.0%: Score 86: DH 2; Length 488: Best Local Similarity 20.0%: Pred. No. 1.1; Matches 87: Conservative 48: Mismatches 127: Indels 174: Baps 24:
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Db	235	IDAVKHIKYSETROWLTHVKNATGKEMFAVAEFWKNULG ALENYLNKTNWN 285
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KEYWORLS SOURCE

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ORGANISM

Mus musculus

house mouse

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AUTHORS

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COMMENT

Contact: George J. Karqul

Laboratory of Genetics

JOURNAL

embryo using a 15,000 monse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

Genome wide expression profiling of mid destation placenta and

National Institute on Ading/National Institutes of Health 833 Cassell Drive, Suite 4000, Haltimore, MD 21224-6820, USA

lanaka.l.S., Jaradat,S.A., Lim,M.K., Karqul,G.J., Wang,X., Grahov,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W. LII, Becker,K.G. and Ko,M.S.H.

Grahovac

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Mammalia; Entheria; Rodentia; Seturognathi; Muridae; Murinae; Mus

FEATURES.

Plate: how z Seq primer: '21M14 Forward High quality sequence stop: 614 Email: cdna*lqsun.qrc.nia.nih.gov Plato: 1.0072 row: G column: 08 Seq primer: ~21M14 Forward

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ligation mixture by chemical method. The library was constructed by xiaobong Wang."

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3.42ig of total RNA. The double stranded cDNAs were treated with 14 INA polymerase and purified by ethanol precipitation. The cDNAs were lighted to Lone Tinker LL-Sal (include Sall sequence). The cDNAs were purified by phenol/chloroform and separated from tree linkers by centricon 100. Then, cDNAs were amplified by long range high fidelity PCR using Takara's Ex Tag polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centricon 100. The cDNAs were digested with Sall and Notlergues. Then, the cDNAs were digested with Sall and Notlergues. Then, the cDNAs were size selected by Gibco's Size Fractionation column. The cDNAs were cloned into Sall/Notl site of pSPsdcl plasmid vector. The DHIOR E. coll lost was transformed with the literature by

/dev_sique-12.5dpc"
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/lab_host="BHIOB"
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2 Mesonephros. The double-stranded cDNA was synthesized
by Gibco's Kit with an olimp(dT) primer [Not]

primer adapter from GibcoBRL]

/elone_Lib "Mouse_El2.5 Female Mesonophros and Gonads etwA Library"

/sex-"temale"

/clone-"L0072G08" /strain "C57BL/6J" /db_xref-"taxon:10090" ∕organism "Mus musculus"

Obery Match (11.7%) Score [37.8; $\rm DB(23)$ Length 614; Host Local Similarity (56.7%) Prod. No. 7.9e (2; Matches 27%) Conservative (0; Mismatches 207; Endels () 521 GOTTOTICTICTICAGTATICCCTCAGGAAAGGTGACCCCAAACTTCGAATGAACATC 462 7.65. atsitsgitteatsjatsganatitgeeeaangeteegangategeeagtiaeaggaaeaagee 795 675 gradaattigitgatagttitgaagggeggttgetexaeeeaggaeaegggaeattgaagee 735 581 GGAAAAGAGYTTCCTGGTTGGGAAGAGACATCAGAACCCAGAGACACACAGAAGCT 521 sdet.

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C78078 Mouse 3.5-dpc blastocyst cDNA Mus musculus cDNA clone
J0042D11 3' similar to Rat mRNA for renin-binding protein, m
                                                                                                                                                                                                                                                                                                                                                    Systematic analyses of genes expressed in 3.5-dpc mouse blastocyst (The ERATO/Doi Project at Wayne State University)
[Inpublished (1997)
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Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
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Japan Science and Technology Corporation (JST)
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/tissuc_type-"blastocyst"
/dev_stage="3.5-dpc"
                                                                                                                                                                                    /strain="C57HL/6J"
/db_xrei="taxon:10090"
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                                                                                                                                                                                                                                                                                                    Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishiay, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
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                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugimoto, Y., Hirotsune, S., Lakasuga, A., Itoh, R., Jitohzono, A.
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                  Location/Qualitiers
                                                                           /dev_stage="letus"
                                                                                                  /clone_lib="Bos taurus kidney
/tissue_type="kidney"
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Washington University School of MedicineP
4444 Forest Park Parkway, Rox 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marria,M., Hiller,L., Allen,M., Rowless,M., Dietrich,N., Dubbque,T., Geisel,S., Kueaba,T., Lary,M., T., Marria,M., Morris,M., Schellenberg,K., Stephoe,M., Tan,F., Underwood,K., Moore,B., Theising,R., Wylie,T., Leunon,G., Soares,B., Wilson,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
Contact: Marra M/Mouse ESI Project
                                                                          Seq primer: 28ml3 revl ET from Amersham
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L. (bases 1 to 449)
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                                                                                                                           vertor to vector length is 450
                                                                                                                                                                      Putative bull length read
                                                                                                                                                                                                                                                 This clone is available royally free through LLNL; contact the IMAGE consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                     Email: mouseestawatson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU HHMI Monse EST Project
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                                                                                                                                                                                AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                      A1070075 497 bp mRNA EST 05 JUL 199 UI-R-Y0-1s c-02-0 UI.SI UI-R-Y0 Rattus norvegicus clNA clone UI-R-Y0 Is-c-02-0-UI-8', mRNA sequence.
                               451 Eckstein Medical Research Building Towa City. IA 52242, USA Tel: 319-335-8250
                                                                                     Contact: Soures, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                            97044477
                                                                                                                                                                                                                                                                                     Rattus norvegicus
Email: msoares⇔blue.weeq.uiowa.edu
                                                                      University of Iowa
                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                              discovery
                                                                                                                                                                            Normalization and Subtraction: two approaches to facilitate gene
                                                                                                                                                                                               Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata: Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae;
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                  Fax: 319 335 9565
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/dev_stage="M30 CD4+ cells"
/lab_host="SOLR_(kanamycin_resistant)"
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/db_xref "taxon:10090"
/clone-"IMAGE:958903"
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Pred. No. 3.9e-28;
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The sequence tag present in the cDNA between the Not1 site and the

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BASE COUNT
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ATGTGCCGCGGTGCCTGGCCATGTGCGAGCAGATTTT 112
                                                                                                                            TGAM CAMGAGGAMAAGGTGGCCTTACCATCAAAGGAGGTCCTTTTAAAGGCTGCTTCC 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host-"DHIOB (Lite Technologies)"
/lab_host-"DHIOB (Lite Technologies)"
/note-"Vector: pf773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1: Site_2: Eco RI: Nic UI:R-YO library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-AO, UI:R-AL, UI-R-EO, pool of all previous libraries (UI-R-AO, UI:R-AL, UI-R-EO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the HI-R-YO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
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/clone_lib="U1-R-Y0"
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/db_xref-"taxon:10116"
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                                                    A1794002 542 bp mkNA EST Danio rerio cDNA 57 similar to SWERNEP_RAT PS1607 RENIN-BINDING PROTEIN ; mkNA sequence.
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Mammalia; Entheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
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KO,M.S.H., Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T., Grahovac,M.J., Mason,S., Lim,M.K., Paonessa,F.D., Sanls,A.D. and
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Japan Science and Technology Corporation (JSI)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Ch
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Washington University School of Medicine
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Sequencing Center Clone distribution: Genome Systems, St. Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        were sequenced additional times to assess quality control."
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Institut ther Molekulare Genetik, Herlin), cDNAs for EST
analysis were selected following oligonucleotide
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gener Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCL CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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DNA Sequencing by: Washington University Genome Sequencin, Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: M. Bento Soares, Ph.D.
                                              - Fatima Bonaldo.
1970 — 12
                                                                                                                                                                                                                                                                           Zhote "Graun: kidney; Vector: pTZT(D Fac (Fharmacia) with a modified polylinker; Site]: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NC1 CGAP Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCK amplified cDNAs
                                                                                                                                                                                    from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325841, 1471368 1472903 and
                                                                                            1492104:1493255). Subtraction by Bento Sources and M.
Fatima Bonaldo. "
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/lab host "DHTOB"
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Best Local Similarity 55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOHRNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 AGCCGAGAGGGCAAGGTGGCCCTTTCCATCAAGGGAGGTCCTTTCAAAGGTTGTTTCCAG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     943 ctauccaauguccaccaauccaggccaagaaaaatuttggcaatugtttgagcgggtc 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                883 coordactaactqqaatqqqarcaaaaqototqqtqqqtacatttqqaaacrotqqttqco 942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITCTTCALGGGTTACAGTGACAGTGGGGGACCTTGTGTTGTTGCGCTTL111TTACCAAGTG 224
                                                                                                                                                                                                                                                                                                                                             Email: msoares blue weeq.uiowa.cdn
The sequence contained an object track that was present in the
oligonneleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonalide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A(575,270) 458 bp mkNA ESI 05-APR-1990 IL R Y0-yc-e-12-0-UI.sl UI-R-Y0 Rattus norvegicus cDNA clone UI-R-Y0-yc-e-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegious
                                                                                                                                                                                                                                                                                              normalized Eye library cDNA Library Preparation: M.B. Soares I
Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A1575270.1 G1:4559646
                                                                                                                                                                                                                                               Seq primer: Ml3 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 319 335 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Normalization and subtraction: two approaches to tacilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
                                                                                                                                                                                                                                                                     Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 358)
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                                                       /Organism="Rattus norvegicus"
/Strain="Sprague-Jawley"
/db_xrei="taxon:10115"
/clone="UI-R-Y0-vc-e-12-0 UI"
/clone_lib="UI-R-Y0"
/lab_host="DH10B (Life Technologies)"
                              /dev_stade-"adult"
                                                                                                                                                                                                                      Location/Qualitiers
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                me44h06.rl Somres mouse panwells,5 Mus musculus chNA clone imAGE:351419 5' similar to PIR:JXO187 JXO187 renin-binding protein
                                                                                                                                                  Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, E., Geisel,S., Kucaba,T., Lacy,M., Je,M., Marthu,J., Morris,M., Schellenkera,K., Steptoe,M., Tan,F., Underwood,K., Moore,H., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Enteleostomi:
Mammalia: Entheria: Rodentia: Scluroquathi: Muridae: Murinae; Mus
1 (bases 1 to 349)
                                                  Unpublishad (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Contact: Marra M/Mouse ESI Project
                                                                                                     The WashU HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amplified chNA inserts from previous library clones from which 3' ESIs had been derived were used as a driver in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of origin of a clone within the mixture. The subtracted library (UI-R-Y0) was constructed as follows: PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            library. The driver for the Subtraction consisted of a pool of all previous libraries (HER-AU, HER-AU, HER-AU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Juster "Vector: pT714D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I: Site_2: Eco RI: The HI R-YU library is a subtracted library deviced from an individually lagged normalized whole-eye (minus the lens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo-dT track which allows identification of the library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 bp
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Pred. No. 1.4e-16;
0; Mismatches 99; Indels 0
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                                                                                                                                                                                                                                                                                               Eukaryota: Metaroa; Chordata; Chaniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Schurognathi; Muridae; Murinae; Mus
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Sources and M.Fatima Honaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
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/dev stage "19.5 dpc total tetus"
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                                                                                 carninei,E. Shibata,K. Osawa,Y. Komo,H. Itoh,M. Aizawa,K.
Akahira,S. Akiyama,L. Fukuda,S. Fukunishi,Y. Funayama,L. Hata
Ak. Hayatsu,N. Hoff,E. Ishikawa,L. Itoh,M. Izawa,M. Kawai,L.
Kikuchi,N. Kojima,Y., Matsuyama,L., Niftsuma,H., Oda,H., Owa,C.,
Safo,K. Shibata,Y. Shiqemoto,Y. Shiraki,T. Soqabe,Y. Suqabara
Y. Sazuki,H. Suzuki,H. Tateno,M., Tomaru,Y. Tominaqa,N.,
Watanabe,S. Yadame,M. Yamamora,J. Yokota,I. Yoshimo,M.
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Froc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using kNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):4455-3460 (1998))
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Single pass sequencing. Bases called and trimmed with phred
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Thermostabilization and thermoactivation of thermodabile enzymes by
trehalose and its application for the synthesis of fall length cDNA
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ULLR CZP-rd-q 06 0-ULLS1 ULLR CZP Rattus norvedicus cDNA clone
ULLR CZP rd-q 06 0-ULLS1 ULLR', mrna sceptonce.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Research denotics (www.resden.com)
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Mammalia; Entheria; Rodentia; Seinrognathi; Muridae; Murinae;
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: 419-435-8250
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/organism "Bos Laurus"
/fb xret "taxon:9914"
/clone lib "MARC 4Bov"
/fissue type="pooled"
/lab bost "DBIOR"
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/elone "UL R C2p rq q 06:0:UI"
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/db xret "taxon:10116"
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62.1%; Pred. No. 2.6e 11;
vative 0; Mismatches 69; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           into DH10H bacteria (Lite Technologies) to generate the ULR C2p Library. This procedure has been previously described (Bonaldo, Lemon and Soares, Genome Research 6:791-806, 1996)"

4 67 c 79 q 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library in the form of single stranded circles. The remaining single stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
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/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/hote "Vector: pt?Fd pac (Pharmacha) with a modified polylinker: Site 1: Not 1; Site 2: Eco kl; The H1 k c²2p library is a subtracted library derived from the UL k c²1 library, which is a subtracted library derived from the UL k cº library consisted of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          embryo. The tag is a string of
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 71.4: DB 11: Length 269: 
Pred. No. 2.9e 11: 
0: Mismatches 51: Indels 0
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Search completed: January 1, 2001, 21:57:17 Job time: 11363 see

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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Regult.	S. Coffe	Match Length DB	Lenyth		ID	Description
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بد	33.5	2.4	2214	_	020383	ADH complex struct
4	33.5		2751	7	Q69001	Product of alterna
্য	44.5	2.3	2751	17	T03625	Alternatively spli
٦	33.6	2.4	2789	15	069000	Product of alterna
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œ	43.5	tu ua	4705	15	866890	Human protocadheri
9	33.6	2.9	4705	17	T03622	Protocadherin clos
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2.5	2.5			6.6	2.6	2.6	2.6			2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7
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142063	X20515	V81946	T14821	194102	T08807	091438	T11708	T08804	Q91439	V54209	2.45875	2.45874	219230	Z19442	X34104	X 34 1 0 3	Z32020	V34683	Z87686	Z87685	246651	X84349	X84332	X36523	Q48939	T10583	261811	Q11434	X33123	V09774	V04777	V88857
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T04122; 09-MAY-1996

(first entry)

s S RESULT T04122

104122 Standard: DNA; 1209 BP

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X	Porcine; acylo	Porcine; acylqlucosamine-2-epimerase; N.acetylmannosamine;
×ε	N-acetylneuran	N-acetylneuraminic acid: renin-binding; enzymatic production:
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Query Match Best Local Similarity

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                        cheoding the 72kD ADH submit was isolated and sequenced. It forms a membrane bound ADH complex with a 44kb sub unit (cytochrome c) whose coding sequence is located immediately downstream of the acquenceding the 72kD sub-unit. See also gless.
                                                                                mixture was used to transform E.coli JM109. Probes were designed based on the N terminal amino acid sequence of the ADH complex isolated from A. alfoaceligenes (see 013082-01308). The gene
Sequence 2214 BP; 451 A; 683 C; 662 G; 418 T; 0 other;
                                                                                                                                  Pst1 and Smal and ligated to Pst1-Smal cleaved pUC18. The ligation
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90JP-0042391
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                                                                                                                                                                       Query Match 2.9%;
Best Local Similarity 53.9%;
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                                                                                                                                                                                                                                                                                          The gene encodes a protein of mol. wt. ca. 72.000. Acetobacter transformed with the sequence can enhance the efficiency of acetic acid fermentation. The ADH complex can be easily extracted from the bacteria and purified and it can be used for the determination of an
                                                                                                                                                                                                                                                                                                                                                                                             Alcohol dehydrogenase complex structural gene - used in plasmid and enhancing efficiency of acetic acid fermentation for transformed acetic acid bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q20383;
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig \beta(1-3); 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; R20192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1990;
26-MAR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q20383 standard; DNA; 2214 BP
                                                                                                                                                                                                                                    Sequence 2214 BP; 452 A; 683 C; 662 G; 417 T;
                                                                                                                                                                                                                                                                                alcohol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NAKA:) NAKANO SUTEN KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 · NOV - 1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP03266988-A
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                                                                                                   872 tyytetaeetyggeyttggeaacgyttegeeytggaactaeaagtaeegtteegaaggea 931
                                                                                                                 707 tyeteaaceeaqqacacggcattgaagccatgtggttcatgatggacattgcccaacgct 766
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                                                                                                                                                                                                                                                               also Q20383-84, and -86-88
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                                                                     coggregal egeragitiaraggageaageeattgeagtggtgtttgaacaccctggaatatg 826
                                          aggycyacaacctqttcctgggcagcatcytcgcactgaagccggaaaccqurgaatacg
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                                                                                                                                                          Score 33.6; DB 13;
Pred. No. 0.9;
0; Mismatches 59;
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                                                                                                                                                                                        Length 2214;
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                                                                                                        Query Match 2.9%;
Hest Local Similarity 45.7%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                            contained the putative entire coding sequences of two novel proteins designated protocodherin-4; proteins designated protocodherin-4; (pc42). The DNA and deduced AA sequences of pc42 are in 068997/R58906, while those of pc43 are in 068998/R58907. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Two tull length human cDNAs corresp. to the partial cDNAs of HUMAN-42 and HUMAN-43 (Q68981,Q68982) were isolated from human letal hrain cDNA library. Several overlapping cDNA clones were isolated with each probe including two cDNAs which
                                                                                                                                                                                                                        sequences of two possible products of alternative splicing of pedamRNA are respectively presented in Q69000/R58912 and Q69001/R49144
                                                                                                                                                                                                                                                                                          consistent with the consensus sequence of mRNA splicing, suggesting that these clones may corresp. to alternatively spliced mRNAs.
                                                                                                                                                                                                                                                                                                                                           analysis of various overlapping protocadherin cDNA clones revealed that some clones contd. unique sequences at the 3' end. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WP1: 1994-293849/36.
P-PSDB; R49144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q69001 standard; cDNA; 2751 BP
                                                                                                                                                                                          Sequence 2751 BP; 698 A; 715 C; 696 G; 642 T; 0 other;
                                                                                                                                                                                                                                                          The DNA and AA sequences of one possible product of alternative splicing of pc42 mRNA are given in Q68999/R58911. The DNA and AA
                                                                                                                                                                                                                                                                                                                              sequences forming the boundaries of the 3' end regions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cadherin; protocadherin; cell adhesion molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Product of alternative splicing of human protocadherin 43 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 99-102; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide sequences encoding new proto:cadherins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DOHE-) DOHENY EYE INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tor modulating natural binding and regulating activities.
362 tegeegeeatggeetttagteaatatgeettageeagtggggegeaggaagetaaageea 421
                                      914 ttgcaacqgatctggatgaaggccccaacggtgaaattatttactccttcggcaqccaca
                                                                       302 tigetitiggaleaggaaggeaaaceeetgegteaaceetataaegtiittiieegaiiget 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (tirst entry)
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Pred. No. 1;
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                                                           these sequences are involved in cell cell adhesion. The proteins may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against the encoded sequences are useful
                                                                                              method from those with a cytoplasmic domain. The p
these sequences are involved in cell cell adhesion.
                                                                                                                                             domain is not present in all cadherins, but in those which possess it, it is essential to the cadherins adhesive function. The cadherins which do
                                                                                                                                                                            cytoplasmic domain of cadherin interacts with the cytoskeleton through catenins and other cytoskeleton associated proteins. The cytoplasmic
                                                                                                                                                                                                               library (contained within lambdaZapII vectors), with 32P labelled versions of the sequences represented by T03605 and T03606. The abundant spliced version of pc42 is represented in T03622. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.X
3.X
3.X
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                                             tor modulating the binding activity of protocadhorins,
                                                                                                                           not possess a cytoplasmic domain appear to function via a different
                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide(s) encoding human protocadherins ped and ped and rat
peb—involved in cell cell adhesion and regulation activities
                                                                                                                                                                                                                                                                                                                                                                                                                       F PSDB; R87154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probocadherin; pe3; pe4; pe5; human; rat; cadherin; cell adhesion; monse; catenin; therapy; clone; troq; truit tly; ss.
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                                                                                                                                                                                                                                                                These sequences were isolated after screening a human toctal brain cDNA
                                                                                                                                                                                                                                                                                 the cDNA clone of the human profocadherin sequence, designated pc43.
                                                                                                                                                                                                                                                                                               T03624 and T03625 represent possible alternatively spliced versions of
                                                                                                                                                                                                                                                                                                                                  Example 4; Page 107 110; 146pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANSHOOT ( SHOOT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 JUN 1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO 46.25;
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                                                                                                            The proteins encoded by
                                             and can be used
                                                                                                                                                                                                                                The most
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Sequence 2751 BP; 698 A; 715 C; 696 G; 642 F; 0 other;

Q68997/R58906, while those of pc43 are in Q68998/R58907. Sequence

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Best Local Similarity 45.7%;
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            contained the putative entire edding sequences of two movel proteins designated protocadherin-42 (pc42) and protocadherin (pc43). The DNA and deduced AA sequences of pc42 are in
                                                                                                                                                                    Two full length human cDNAs corresp. to the partial cDNAs HUMAN 42 and HUMAN 43 (Q68981,Q68982) were isolated
                                                                                                                                                                                                                                                                                                                                                           Polynucleotide sequences encoding new proto:cadherins
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cadherin; protocadherin; cell adhesion molecule; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q69000 standard; cDNA; 2789 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clones were isolated with each probe including two conas which
                                                                                                                                   from human fetal brain cDNA library. Several overlapping cDNA
                                                                                                                                                                                                                                                                                                                                 for modulating natural binding and regulating activities
                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; R58912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suzuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Product of alternative splicing of human protocadherin 4+ mkNA
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                                                                                                                                                                                                                                                                 Example; Page 94:96; [14pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-080-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 thycochacagacchacaahacghechacaccateagcacaaheccaaagahcaahaca 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       914 tigeaacygatetqgatgaaggeecaacygtgaaattatttacteetteggeageeaca 973
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Prod. No. 1;
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RESULT
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Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analysis of various overlapping protocadherin cDNA clones revealed that some clones could, unique sequences at the 3' end. The sequences forming the boundaries of the 3' end regions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1154 acadegeeeeggagat 1169
                     P-PSDB; R87154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protocadherin: pc3; pc4; pc5; human: rat; cadherin; cell adhesion; catenin; therapy; clone; troq; truit fly; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103624 standard; cDNA; 2789 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.94 annoncedal recharged are all the state of the st
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                                                            WP1; 1996-068874/07.
                                                                                                                               Suzuki S;
                                                                                                                                                                                           (DOME) DOMENY EYE INST
                                                                                                                                                                                                                                                                  27 - JIJN - 1444;
                                                                                                                                                                                                                                                                                                                              26-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                     04 - JAN 1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₩09600289 Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternatively spliced pc43 coding sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T04624;
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115..2625
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45.78;
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Pred. No. 1;
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PT Polynucleotide(s) encoding human protocodherins pet and pet and rat PT pc5 - involved in cell cell adhesion and regulation activities XX pc5 - involved in cell cell adhesion and regulation activities XX pc5 - involved in cell cell adhesion and regulation activities XX pc5 - involved in cell cell adhesion and regulation activities of CC the cDNA clone of the human protocodherin sequence, designated pc4. CC These sequences were isolated after screpting a human fortal brain cDNA CC library (contained within lambdaZapii vectors), with 32P labelled CC cytoplasmic obmain of pc42 is represented in 103622. The cc stone of the sequences represented by 103605 and 103606. The most CC domain spliced version of pc42 is represented in 103622. The cc cytoplasmic domain of cadherins interacts with the cytoskaleton through CC catenins and other cytoskaleton associated proteins. The cytoplasmic Comain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cytoplasmic CC mot possess a cytoplasmic domain appear to function via a different cc method from those with a cytoplasmic domain. The proteins encoded by these sequences are involved in cell-cell adhesion. The proteins may properties. An ibodies produced against the encoded sequences are useful cc for modulating the binding activity of protocadherins, and can be used the rapeutically.

XX Sequence 2789 BP; 615 A; 781 C; 761 G; 642 T; 0 other:
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Ouery Match 2.98;
Host Local Similarity 45.78;
Matches 117; Conservative
1154 acaacyceceqqagat 1169
                                                                                                   1094 aygycychatceegaaggaycacattycaaaytyttygtygayyttytgaatytyaaty 115
                                                                                                                                                                                                  1034 agggteggetggaettrqaggaearcaaaaetecatgagatttarateraqqreaaagara 109
                                               542 accteaecctydagat 557
                                                                                                                                                                                                                                                                                                     974 adegegeeggegtgeggegaetattegeettagaeettgtaacegggatgetgaeaatea
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Pred. No. 1;
U; Mismatches 139;
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ULT 8
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Q68998 standard: cDNA: 4705 EP.
Q68998;
17-APK-1995 (first entry)
Human protocadherin: cell adhesion molecule: ss
Cadherin: protocadherin: cell adhesion molecule: ss
Homo sapiens.
Key
Location/Qualifiers
CDS
115..2827
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07 - JUL - 1994

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Best Local Similarity 45.7%;
Protocadherin; pes: pes; pes; human; rat; cadherin; cell adhesion; mouse; catenin; therapy; clone; trog; fruit fly; ss.
                                                                                                          Protocadherin clone 43 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (pc43). The DNA and deduced AA sequences of pc42 are in 068997/R58906, while those of pc43 are in 068998/R58907. The overall structures of pc42 and pc43 are similar to that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W|.;
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                                                                                                                                                                                  29 AUG 1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and pc42 contains seven subdomains that closely resemble the typical cadherin extracellular subdomain while pc43 has six such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           typical cadherins but they do have distinct features. Both lack
the prosequences that are present in all known cadherin precursors
The extracellular demains of pc42 and pc43 are different in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from human fetal brain cDNA library. Several overlapping cDNA clones were isolated with each probe including two cDNAs which
                                                                                                                                                                                                                                                                      TU $5.227
                                                                                                                                                                                                                                                                                                                                       10.6522 standard; cDNA; 4705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1154 acadegeeeeqqaqat 1169
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The protein encoded by this sequence is involved in cell cell adhesion. The protein may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Folynucleotide(s) encoding human protocadherins pet and pc4 and rat
pc5—involved in cell-cell adhesion and regulation activities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4705 BP; 1050 A; 1393 C; 1245 G; 1017 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protocadherins, and can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytoskeleton through catenins and other cytoskeleton associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence, designated pc43. This sequence was isolated after screening human foetal brain cDNA library (contained within lambdaZapII vectors).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 79-84; 146pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 JUN 1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04 JAN 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The cytoplasmic domain is not present in all cadherins, but in those
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with 32P labelled versions of the sequences represented by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a cDNA clone of the human protocadherin
                                       542 acctoroctiquadat 557
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                                                                                                                                                                                                                                             914. Et geaacquat et gyat gaaggeeeeaacgyt gaaat talt tilaet eet teggeageeaca. 973
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                                                                                                                                                                                                                                                                                                                                                                                                                               2.9%;
45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modulating the binding activity of
                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 139; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33.5; DB 17; Length 4705;
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Best Local Similarity
Matches 56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                 surarry, and establishment of vascular networks in transplanted cells and tissues. Zapol is also useful as a research agent, such as in the expansion of hematopoietic cells (including stem cells) and endothelial cells. The polypeptides are added to tissue culture media for these cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins may be used therapeutically to stimulate revascularization of tissue. Specific applications include treatment of full-thickness skin wounds, including venous stasis ulcers and other chorde, non-healing wounds, as well as fracture repair, skin grafting, reconstructive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human growth factor designated zapol. Zapol is an analopoietin homologue. The polypeptide is used to stimulate cell growth and tissue development. The polypeptides form multimeric proteins. Zapol has angiogenic or hematopoietic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-1999 (lirst entry)
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 54; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Désenerate DNA encoding a human growth factor designated zapol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a novel andiopoletin homologue, and related DNA, useful for
                                                                                                                                                                                                                                                                                                                                            1218 BP; 182 A; 152 C; 224 G; 132 T; 528 other;
                                                                                                                                                                                                                                                         Conservative
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T58681/c
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                                                                                                                                                                                                   Query Match 2.8%;
Best Local Similarity 49.4%;
                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes a human GPPase-activating protein (196API). The protein has an "IO motif" which is defined as an amino acid sequence of 20-40 amino acids in length containing an isolencine residue immediately collowed by a glutamine residue which has at least 50 percent sequence similarity to the consensus sequence shown in W18823. The DNA sequence used for production of recombinant 196API, which is useful in the diagnosis and treatment of tumours characterised by aberrant ras
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                                                                                                                                                                                                                                                                                                                    expression. Detection of mutations in the 10GAP1 gene is diagnostic of cancer. The 10GAP1 protein can be used for treatment of cancer to reduce the activity of p21-ras. Detection of meoplastic cells can be achieved by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding GIPase-activating protein IQGAPL - for producing recombinant protein useful for tumour diagnosis and therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQGAP1: human G1Pase-activating protein; (v motif: diagnosis: treatment;
tumour: suppressor: ras: cancer; p21-ras; neoplastic cell; ds.
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                                                                                                                                                                                                                                                                      Sequence 7573 BP; 2320 A; 1570 C; 1680 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Column 21-28; 35pp; English
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                                                                                                                  1872 ATTCCAATGCCCTGTTGATCAGGCCCACCGATGACAACATCTCCCACTGCGACAGAGAGCT 181
                                                                                                                                  852 attitafiteetigatryoeagygerarreteeecaacactggaatgggaecaaaaget 911
              972 agaaaaatgttggcaatggtttgagcgggtccatgattacgcctggagtcat
                                                                                 912 ctuqtquqtacatttquaaaccctqqttqccctaqccaaqqqccaccaaqccactqqcca
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Location/Qualifiers
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Pred. No. 3.4;
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                                                                                                                                                                                                                                                                      2003 1; 0 other;
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Indels
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less local Similarity 51.0%; Fred. No. 2.5;
Matches 11; Conservative 0; Mismatches 14; Indels 0;
VHHH5/;
                                   VBBB57 standard; cDNA; 775 BP
                                                                                                                                                                                                                  Claim 1: Fig 4: 21pp: Japanese
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F PSDR: R15470.
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                                                                                                                                                        Sequence 3496 BP: 585 A; 1197 C; 1213 C; 501 T; 0 other;
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(HDSE) HISSIA SHOYEKK
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Overy Match 2.7%; Score (2.2; DB 20; Length 77%; Best Local Similarity 49.1%; Pred. No. 1.4;
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                   Expressed sequence tag; secreted protern; harmatoporesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; ESI; human; chemotaxis; chemokinesis; harmostaxis; gene therapy; thombalysis; receptor; ligand; anti inflammatory; tumour inhibitor; ds.
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                                                                                                                                                                                                                                                                                                                                     forms of HMurroSK which may be associated with a dysfunction and can define a diagnosis of a disease (or susceptibility to a disease) resulting from altered HMarcoSR expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This partial cDNA sequence encodes a novel human Macro scavenger receptor (HMacroSR). This polypeptide and resulting antibodies can be used to treat cardiovascular diseases, including atherosclerosis, hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Marco scavenger receptor - used to develop products for
treating e.g. cardiovascular disorders, septic chock, bacterial
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             1020 teathregeegaateetgagtatggggaatggtttggeetaeetgaateegeeggg 1072
                                                                                                                                                                                                                                                                                                                                                                                         gram positive bacteria. Agonists and antagonists may also be used to treat these diseases. The polynucleotide can be used to detect mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fiq 4; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections etc.
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                                                                                                                                                                                                                                                                                                     Sequence 1560 BP; 389 A; 387 C; 533 G; 251 f; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             failure, endotexaemia and infections caused by gram negative and
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/note= "partial ma
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                                                                                                                                                                                                                            2.7%; Score 42.2; DB 19; Lenath 1560; 49.1%; Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          host detense disorders, septic shock, pancreatitis, multiple organ
tailure, endotoxaemia and intections caused by gram negative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treat cardiovascular diseases, including atherosclerosis, hypertension myocardial and cerebral infarction, angina, organ failure, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Marco scavender receptor - used to develop products for
treating e.g. cardiovascular disorders, septic chock, bacterial
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23-MAY-1996;
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1020 teatilegeegateetgagtatugggaatugttiggetaeetgaategeeggg 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1703 BP; 437 A; 423 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gram positive bacteria. Agonists and antagonists may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gangrene, and loss of function in the extremities. They can also be used to treat or diagnose various macrophage and other immune cell related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Pages 31-32; 45pp; English
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define a diagnosis of a disease (or susceptibility to a disease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treat these diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resulting from altered HMarcoSR expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agonist; antagonist; dysfunction;
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SUMMARIES

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No.	Score	Mat ch	Length	DB	ID	Description	
	134.2	11.4	1209	2	US-08-553-703A-5	Sequence 5, At	Appli
2	134.2	1.1	1209	2	-08-553-703A-	. ئ	Appli
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2	34.5	2.3	2751	_	US-07-998-003A-106	106	App.
7	33.6	2. 4	2751	_	US-08-453-274H-106		App.
œ	33.5	2.4	2751	2	US-08-453-695A-106	Sequence 106,	APP.
ĵ,	34.6	2.3	2751	Ν.	US-08-268-161A-106	Sequence 106,	App
10	33.6	2.9	2751	سه	US-08-453-702A-106	-	94 <u>4</u>
11	33.6	2.5	2751	6	PCT-US93-12588-106	_	App
12	34.6	2.9	2751	5	PCT-US95-08071-106		App
	33.6	2.4	2789		US-07-998-003A-104	Sequence 104.	App
-4	43.6	2.4	2789	_	US-08-453-274H-104	Sequence 104,	App
<u>_</u> ,	33.6	2.4	2789	ν,	US-08-453-695A-104	Sequence 104,	App
16	33.6	2.4	2789	2	US-08-268-161A-104		App
17	33.6	2.9	2789	ند	US-08-453-702A-104	Sequence 104,	App
18	33.6	2.9	2789	2	PCT-US93-12588-104	Sequence 104,	۵pp
19	33.6	2.9	2789	φ	PCT-US95-08071-104	Sequence 104,	App
20	33.6	2.9	4705	_	US-07-998-003A-96	46, 1	Iddy
21	33.6	2.4	4705	_	US-08-453-274H-96	96,	Idde
22	33.6	2.9	4705	Ν	US-08-453-695A-96	96,	Appl
23	33.6	2.9	4705	Ν	US-08-268-161A-96		1ddv
24	33.6	2.9	4705	نین	US-08-453-702A-96	96,	Appl
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TITLE OF INVENTION: EPIMEKASE
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RESULT 3
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         GENERAL INFORMATION:
APPLICANT: MARU, ISAFUMI
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/553,703
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465 teecaaaygteaatacgagaagteetateeaggtactagaceeeteaaateeetgyeggt
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STRANDEDNESS: single
TOPOLOGY: linear
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REGISTRATION NUMBER: 34
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SOFIWARE: FastSE
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                                       ACGGTACCAGAGCGAAGCGGTGGACATGATGGATCAGATCGTGCACTGGGTGCGAGAGAGGA 482
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620 Newport Center Drive 16th Floor
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TELEPHONE: 714-760-0404
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ALLORNEY/AGENI INFORMATION:
NAME: Altman, Daniel E
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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663 TGGACAGGCTGTGCTGGAGAATGTGTCGGAAGATGGCGAGGAACTTTCTGGCTGCCTGGG
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GENERAL INFORMALION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANI: Kawdmura,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
                                     FILING DATE: 26-MAR-1990 AUTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72 mb
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APPLICATION NUMBER: US 07/658,;
FILING DATE: 20-FEH-1991
APPLICATION NUMBER: 73440/1990
                                                                                                                                                                                                                     CURKENI APPLICATION DATA:
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SIAIE: New Tork
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                                                                                                                                                            CLASSIFICATION: 435
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REGISTRALION NUMBER:
                      NAME:
                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                    APPLICATION NUMBER: US/07/985,458
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Fukaya, Masahiro;
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                    Herbert
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Containing The Same And Transformed Acetic Acid
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                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                      APPLICANT: Suzuki, Shintaro
THILE OF INVENITOR: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 107
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PAGES: 292-34
*TE: 1991
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE
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                                                                                                                                                                                                                                                                                                                                                                                       827 certuguat 834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                             COUNTRY:
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TuPoLogY: ur
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TELEFAX: (212) 870-1622
                                                                                                 STATE:
                                                                                                                                            ADDRESSEE:
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                                                                                                                             STREET:
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EDNESS: double
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Cloning and Sequencing of the Gene Cluster
Eurodina Two Subunits of Membrane-Bound
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                                                                                                                             20 South Clark Street
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Kawamura, Yoshiya;
                                                                                CISA
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Fukaya, Masahiro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tayama, Kenji;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochimica et Biophysica Acta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishiyama, Makoto;
Horinouchi, Sucharu and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lakemura, Hiroshi;
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                                                                                                                                              Bicknell
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53.9%: Pred. No. 0.4;
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                   CURRENT APPLICATION DATA:
                                                                                                                          COMPUTER READABLE FORMS
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                                                                                                                                                                                                                                                                                                               APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocac
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                                                                                                                                                                                                                                                                                               NUMBER OF SECHENCES:
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                                           SOPTWARE:
                                                          MEDIUM TYPE: Floppy disk computer: IBM Pr compatible operation system: Pr poszms-bos
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SIRANDEDNESS: single
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    ADMINISTRATION NUMBER
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                                                                                                                                                  6,05,05, 6,402
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                                                                                                                                                                                                                              98: Marshall, O'Toole, Gerstein, Murray & Borun
6400 Sears Tower, 233 South Wacker Drive
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: Patent No. 5708143
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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AITORNEY JASENI INFORMATION:
NAME: NO. 5663300Jand, Greta E.
REGISSTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32660
TELECOMMUNICATION INFORMATION:
ALTORNEY/AGENT INFORMATION
                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                 COMPUTER READABLE FORM
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                    CLASSIFICATION:
                                                                                                       MEDIUM IYPE: Floppy disk
COMPULER: IHM Pr compatible
OPERALING SYSTEM: Pr DOSAMS DOS
SOFIWARE: Patentin Release #1.0, Version #1.25
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                                           FILING DATE:
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LOCALION: 115
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                                                              US/08/454,695A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 106, Application US/08268161A Patent No. 5798224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 117; Conservative
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INFORMATION FOR SEQ ID NO: 106:
                                                                                                                 COMPHIER READABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: FROM POCOMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CORRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
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LENGTH: 2751 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1154 ACAACGCCCCGGAGAI 1169
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LOCALION: 115..2160
                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Mirshall, O'Toole, Gerstein, Muiray, & ADDRESSEE: Borun
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REGISTRATION NUMBER: P-41,337
                     NAME:
                                                                                                      APPLICATION NUMBER:
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                                                                                June 27, 1994
                                                                                                        US/08/268,161A
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; Patent No. 5891706
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Jisk
COMPUTER: IFM For compatible
OPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Protocadherin Materials and Merri
NUMBER OF SEQUENCES: 115
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TELECOMMUNICATION INFORMATION:
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                                                         ATTORNEY/AGENT INFORMATION:
NAME: No. 5891706and, Gr
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TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: single
                                                                                                 CLASSIFICATION: 435
                                                                                                                            FILING DATE
                                                                                                                                              APPLICATION NUMBER: US/08/453,702A
                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                           STATE:
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                    REFERENCE/DOCKET NUMBER: 32657
                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                60606
                            No. 5891706and, Greta E. TRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                        Hilinois
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Rest Local Similarity 45.7%;
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                                                                        FILING DATE: 29 DEC 1992
ATTOHNEY/AGENT INPORMATION:
                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                        COMPUTER REALABLE FORM:
MEDIUM TYPE: Flophy disk
COMPUTER: INM PC popy disk
COMPUTER: INM PC popy disk
COMPUTER: PATENT PC DOS/MS: DOS
SBETWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suzuki, Shintaro
THTLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 107
TELLECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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LENGTH: 2/5] base pairs
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                                    NAME: Noland, Greta E. REGISTRATION NUMBER:
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               REFERENCE/INSTRET NUMBER:
                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
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LOCATION: 115...2160
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TELEFAX: 312/474 0448
TELEX: 25 4856
                                                                                                                     APPLICATION NUMBER:
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STRANDEDNESS: single
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                                                                                              29 DEC 1992
                                                                                                                     US 07/998,003
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                                45, 402
                 0; Mismatches 189; Indels 0; Gaps
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; LOCALTON: 115
PGI US93 12588-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 106, Application PC/TUS9508071
GENERAL INFORMATION:
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Best Local Similarity 45.7%;
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                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                     AITERNEY/AGENT INFORMATION:
                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Protocadherin Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1094 AGGGCGCCAATCCCGGAAGGAGCACATTGCAAAGTGTTGGTGGAGGTTGTGGATGTGAATG 115
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                                                                                                     FILING DAIR:
                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible COMPUTER: PC DOS/MS DOS
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                      APPLICATION NUMBER: US 07/998,003 FILING DATE: 29 DEC 1992
                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1ENOTH: 2751 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US95/08071
                                                                                                                                                                                                                                               SOFTWAKE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun
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TELEFAX: $12/474-0448
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Notand, Greta E.
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Pred. No. 0.45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 106:
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REFERENCE/DOCKET NUMBER: 32
LELECOMMUNICATION INFORMATION:
                                                                                                                                                  SOFTWAKE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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LENGIH: 2751 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EILLE OF INVENTION: Protocadherin Materials and Methods NUMBER OF SEQUENCES: 107
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                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERALING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 115..2160
                                                                                                     APPLICATION NUMBER: FILING DATE:
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                      REGISTRATION NUMBER:
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REFERENCE/DOCKET NUMBER:
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                  No. 5643781and, Greta E. RATION NUMBER: 35,302
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20 South Clark Street
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                                                                                                                                                                                                                                                                                                                      STREET: Chicago
CITY: Chicago
TMATE: Illinois
                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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LENGTH: 2789 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS DOS
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TELEPHONE: 312/...
""" """ 332/984-9740
                                                                                                                                                    FILING DATE:
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LOCATION: 115
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                                                                         REFERENCE/DOCKET NUMBER:
                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                               MEDIUM TYPE:
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TELEX:
                 TELEFAX:
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25-3856
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6300 Sears Lower, 233 South Wacker Drive
                 312/474-0448
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                INFORMATION FOR SECTIONS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADERESS:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                              NAME: NO. 570814 and, Greta E.
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                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: 10-DOS/MS-DOS
SCETWARE: Patent In Release #1.0, Version #1.25
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                                    TELEX:
                                                    TELEFAX:
                                                                                                                                                                                                                APPLICATION NUMBER: US/08/453,695A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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LOCATION: 115...2622
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FYPE: meloic acid

STRANGENESS: single
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                                                                                                                                  REGISTRATION NUMBER:
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TYPE: nucleic acid
STRANDEDNESS: single
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Search completed: January 1, 2001, 22:21:59 Job time: 12635 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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P13685 escherichia	PU5803 intluenza a	P21951 saccharomyc	Q59749 rhizobium m	Q978m3 chlamydia p	P38016 chlamydia m	P53008 saccharomyc	Q92178 gallus gall	P15057 bacteriopha	-	Püss61 dietyoglomu		Q29451 bos caurus		Р75368 mycoplasma	P46944 saccharomyc	©43280 homo sapien			P46214 pyrococcus	P27033 pseudomonas				053175 mycobacteri				_		-	P51607 rattus norv	P17560 sus scrofa	Description	

P20906 pseudomonas	P20906	MDLC_PSEPU		528	3.8	82.5	ū
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9 bacteriopha	P07659	RPOL_BPT3	1	884	ي. ي	83	-
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P04954 clostridium	P04954	GUND_CLOTM	_	649	٠. 9	83	99
or yet olaqus	P19813	TREA_RABIT		578	3.9	83	œ
neurospora	Q01291	RSO_NEUCR	_	293	3.9	83	7
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s SWISS-PROT entry is copyright. It is produced through a ween the Swiss institute of Bioinformatics and the PMHH. European Bioinformatics institute. There are no restrictly non-profit institutions as long as its content is by non-profit institutions as long as its content is littled and this statement is not removed. Usage by and I itles requires a license agreement (see http://www.isb-sit	THE AMOUNT BEING MUCH GREATER IN KIDNEY THAN IN THE OTHER TISSUES.	1 7	ACTIVITE ACTIVITY: N-ACETYL-D-GLUCOSAMINE - N-ACETYL-D- - I- CATALYTIC ACTIVITY: N-ACETYL-D-GLUCOSAMINE - N-ACETYL-D- MANNOSAMINE.	-i- FUNCTION: CATALYZES THE INTERCONVERSION OF N-ACETYLGUCOSAMINE TO N-ACETYLGUCOSAMINE. BINDS TO RENIN LORMING A PROTEIN COMPLEX CALLED HIGH MOLECULAR WEIGHT (HMW) RENIN AND INHIBITS RENIN ACTUALY.	morecular croming and reconstruction of wary) in approximate 2-epimerase from porcine kidney as a renin-binding protein.": J. Biol. Chem. 271:16294-16299(1996).	MEDLINE: 96279179. Maru I., Ohta Y., Murata K., Tsukada Y.;	TISSUE-KIDNEY CORTEX:		Theorems, december 1997 the formation of an RuBP-remin heterodimer and an relationship to the formation of an RuBP-remin heterodimer and an	LEUCINE-ZIPPER, AND MUTAGENESIS. MEDITINE: 91268065. TOOLO H. TAKABASHI K. BURNI K. MINAKA K.	J. Biol. Chem. 265:6556-6561(1990).	Indue H., Fukui K., Takahashi S., Miyake Y.: "Molecular clouding and sequence analysis of a cDNA encoding a poscine "Molecular clouding and sequence analysis of a cDNA encoding a poscine	OMO JAO JO	AND RECHEMOTE OF A-10 AND 206-250	newer. Sus scrofa (Pig). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	01-AUG-1990 (Rel. 15, Greated) 01-AUG-1990 (Rel. 15, Last sequence update) 30-MAY-2000 (Rel. 15, Last annotation update) N-ACYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.8) (GLONAC 2-EPIMERASE) (N-ACYLGLUCOSAMINE 2-EPIMERASE) (RENIN-BINDING PROTEIN) (RNEP).	LT 1 _PIG _PIG STANDARD; PRT; 402 AA.

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Hest tweat Similarity 44.8
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(ada M. Takabashi S., Miyano M
"Lissue Specific regulation of
10 rats.")
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"Genetic and molecular properties of human and
proteins with reference to the function of the
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or send an email to license/isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJINE; 99145489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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MIM; 312420; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: N-ACETYL-D-GLUCUSAMINE - N-ACETYL-D-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME KEGULATION: A CATALYFIC AMOUNT OF ALP IS GLONAC 2-EPIMERASE ACTIVITY.
PATHWAY: N-ACELYL NEURAMINIC ACTO BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: CATALYYES THE INTERCONVERSION OF N-ACETYLGLUCOSAMINE N-ACETYLMANNOSAMINE. BINDS TO KENIN FORMING A PROTEIN COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MANNOSAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CALLED HIGH MOLECULAR WEIGHT (HMW) RENIN AND INHIBITS KENIN
                   EWEGYLNERGEVILLNI.KGGKWKGCEHVPRALWI.CAETL
                                                                                                                                                                                                                                                                                     SECTY IMAMNELWRATGEVRYQTEAVEMMDQ IVHWVQEDASGLGRPQLQGAPAAEPMAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                     KERETLQAWKERVÖQELDRVVAFWMEHSHDOEHGGFF1CLGREGRVYDDLKYVWLDGRQV 62
                                                      DADNECTTQLEWAMKLWWPHSEAMIAFLMGYSDSGDPVLLRLFYQVAEYIERQFRDPEYG
                                                                                           DROGHEPOOLEWDOKLWWYHLETLVALAKGHOATGOEKCWQWFERVHDYAWSHFADPEYG
                                                                                                                                  PGCLGROONPGH LLEAGWELLRHCTRKGDPELRAHVTDKFLLLPFHSGWLPDHGGLFYFO
                                                                                                                                                                      DSFEGRLLNPGHGIEAMWFMMDIAQRSGDRQLQEQAI-AVVLNTLEYAWDEEFGGIFYFL
                                                                                                                                                                                                                                                MILANLILEMEWILPPHIVEEVLAQIVKEV-----MIDFLDPEIGLMKEAVTPIGEFV
                                                                                                                                                                                                                                                                                                                        STREEAAMARSOYALASGAGRAKATALOAYNNYLR-ROHNRKGOYEKSYPETRPLKSLAVR-176
                                                                                                                                                                                                                                                                                                                                                             WMYCKLYRIFERFRHAGILIDAAKAGGEFILRYARVAPPGKKCAFVLIRIGRPVKVQRTIF 122
                                                                                                                                                                                                                                                                                                                                                                                                WQFAVFYNKLE--PKPQWLEIARHJADFLARHGR--DQDGNWYFALDQEGKPLRQPYNVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RROELAGOYYÓALHOD - - - VLPFWEKYSLDROGGGYFTGLDRKGGVEDTDKFTWLONROV 61
                                                                                                                                                                                                           MMILINLVEGI.--:- GEADEELAGKYAELGDWCARRILQHVGRIGQAVI ENVSEGGKEL
1H5 206 I
417 AA; 47746 MW;
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34.7%;
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Pred. No. 1.1e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 163;
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                       386
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leucine zipper
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P29954;
O1-APR-1994 (Rel. 2
O1-APR-1994 (Rel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for common entitles requires a license of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1994 (Rel. 25, Last sequence update)
30-MANN-2000 (Rel. 39, Last annotation update)
MANN-SE-6-PHOSPHATE ISOMERASE (EC.5.4.1.8) (PHOSPHOMANNOSE ISOMERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium meliloti (Simorhizobium meliloti).
Baeteria: Proteobarteria: alpha subdivision: Rhizobiaceae group:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 122:35-43(1992).
-!- CATALYTIC ACTIVITY: D-MANNOSE 6-PHOSPHATE - D-FRUCTOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt M., Arnold W., Niemann A., Kleickmann A., Phehler "The Rhizobium meliloti pmi gene encodes a new type of pho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE; 93083993.
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or send an email to license*isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: NONE, TO OTHER MANNOSE-6-PHOSPHATE ISOMERASES
                                                                                                                                                                                                                                                                                                               133
                                                                                                                                                                                                                                                                                                                                                     135
                                                                            292 DESVADPTARLWPQTEWLKAAIRFAALTEG
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                                                                                                                                                                                                                                                                         LLPPTTVEEV------LAQTVREVMTD-FLDPEIGLMRE: ----AVTPTGEFVDSFEG 244
                                                                                                                                                                                                                                                                                                               ERGAEMV - - - GRSDKLRRQLEARCKHPLAGFEEDDPPRLPLGS - - · · · ·
                                                                                                                                                                                                                                                                                                                                                   AQEAKATALQAYNNVLRRO-----HNPKGQYEKSYPGTRPLKSLAVPMILANLITEM-EW
                                                                                                                                                                                                                                                                                                                                                                                          WRTAAEGGLLYFDRYYG--QPGGFYGALANADGKLIDASFDLYNQAFALLAFAIILAEVLF 132
                                                                                                                                                                                                                                                                                                                                                                                                                              WEELARHGADFLAR - HGRDQDGNWYFAL - DQEGKPLRQPYNVFSDGFAAMAESQYALASG - 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDAALPLWROKGFDGEGGGEVETTDMKGEPTRDDRKSRVQPROVYCEAA-AGKKGWDGD-74
                                                                                                                   DRQGHPPQQLEWDQKLWWVHLETLVALAKG
                                                                                                                                                     RIVEPGHLEEWAWLLLRWAERRGN----AQAIVKARRLEETGEKDGTOPDRDVVVMILED
                                                                                                                                                                                            RLLNPGHGIEAMWFMMDTAGRSGDRQLQEQAIAVVLNTLEYAW-----DEEFGGIFYFL 288
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27.0%; Fred. No. 1.5e-09;
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01 off 1994 (Rel. 40, Created)
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                                                                            DISLIVE TVAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01 001 1894 (Rol. 27, Created)
15 182 1898 (Rol. 37, Last segmence update)
15 182 1898 (Rol. 37, Last semiotation update)
16 182 1898 (Rol. 47.4 KDA PROTEIN IN GLNA RON INTERGENIC REGION.
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                                                                        STANDARDS
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21.1%;
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by Pred. No. 4.4e-05;
63; Mismatches 166
                                                                                                                                                                                                                                                                                                                                      GOYHYDR 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMTDELDREIGLMRE- AVTPTGEEVDSFEGRLLINDG 240
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4.6%; Score 98.5; DB 1; Length 689;
Hest Local Similarity 21.1%; Pred. No. 1.2;
Matches 55; Conservative 47; Mismatches 100; Indexs 5
                                                                                                                                                                   1046442

10 MAY 2000 (Rel. 49, Created)

10 MAY 2000 (Rel. 39, Last sequence update)

10 MAY-2000 (Rel. 39, Last annotation update)

12 MAY-2000 (Rel. 39, Last annotation update)

12 MAY-2000 (Rel. 39, Last annotation update)

12 MAY-2000 (Rel. 39, Last annotation update)

13 MAY-2000 (Rel. 39, Last annotation update)

14 MAY-2000 (Rel. 39, Last sequence update)

15 MAY-2000 (Rel. 39, Last sequence update)

16 MAY-2000 (Rel. 39, Last sequence update)

17 MAY-2000 (Rel. 39, Last sequence update)

17 MAY-2000 (Rel. 39, Last sequence update)

18 MAY-2000 (Re
                                                                                         Felis silvestris catus (Cat).
Enkaryota: Metazoa; Chordata; Chaniata; Vertebrata; Enteleostomn
Mammadia; Entheria; Carnivora; Fissipedia; Felidae; Felis.
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EMBL: Z99124; CAB16119.1;
SUB11LIST; BG10D4D; YYAL.
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ol-NoV 1997 (Rel.
HYPOTHELLOAL 78.8
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                                 SEQUENCE
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or send an email to licensewisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 DEEFGGTEYFILDROGHPPOOL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456 LLTDGRVMVRYRDGEVKNKGFTDDYAFLLWAYLDLYEASEDLSYLQKAKKLIDDMTSLEW
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KDA PROTEIN IN TELB-EXOA INTERGENTY KEGTON

    Last sequence update)
    Last annotation updat

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-I: FUNCTION: NECESSARY FOR THE CATABOLISM OF N-LINKED CARBOHYDRATES RELEASED DURING GLYCOPROTEIN TURNOVER (BY SIMILARITY).

-I: CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING ALPHA-D-MANNOSIDES.
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Biochem. J. 328:863-870(1997).
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    01 - NOV - 1997
                                             P80888;
                                                                  HCY_PALVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Glycosidase; Glycoprotein; Lysosome; Zymogen; Signal, SIGNAL 1 50 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PIM: PROCESSED INTO 3 PEPTIDES OF 72 KDA, 41 KDA AND 12 KDA -!- DISEASE: DEFECTS IN MANN ARE THE CAUSE OF LYSOSOMAL ALPHA-MANNUSIDUSIS, A LYSOSOMAL STORAGE DISEASE CHARACTERIZED BY ACCUMULATION OF UNBRANCHED OLIGOSACCHARIDES CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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hes 75; Conserv
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                                                                                                                                                                                                                             -----KCWOWFERVHDYAWS-----HFADPEYGEWFGYLNRR 357
                                                                                                                                                                                                                                                                            TMGSDFQYE - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license agreement (So an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ALDQEGKPLRQPYNVF-SDCFAAMAESQYALASGAQEAKATALQAYNNVL--RR
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(Rel.
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                                                                    STANDARD;
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AAB97733.1;
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35, Created)
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18.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 97.5; DB
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51; Mismatches
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                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                  - EDRRSPEYNAEELVNYFLQLATAGGGHERTNHT IM
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Query Match
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DB 1; Length 657;

Matches

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"Primary structure of hemocyanin from Palinurus vulgaris.":
Comp. Biochem. Physiol. 115B:243-246(1996).
-!- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
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PROSITE: PS00498; TYROSINASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: IT CONSISTS OF AT LEAST FOUR VERY SUBCEILULAR LOCATION: EXTRACELLULAR. TISSUE SPECIFICITY: HEMOLYMPH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EACH SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALL THE SUBUNITS
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39, Last annotation
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O5-(475)
40 MAY 2000 (Rel. 9), Created)
40 MAY 2000 (Rel. 9), Last sequence update)
40 MAY 2000 (Rel. 9), Last annotation update)
VALYE TRNA SYNTHETASE (EC 6.1.1.9) (VALINE TRNA LIGASE) (VALES)
VALS OF RYA44H" OF MIY00B.04C.
      PEAM: Proofes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in-
modified and this statement is not removed. Usage by and for ex-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBE outstation—the European Bioinformatics Institute. There are no restriction—on its
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Nature 998:57-544(1998)
! CALALYTE ATPLIFY ATP + L VALINE + TRNA(VAL)
PYROPHOSPHATE + L VALIL TRNA(VAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       send an email to license isb sib.ch)
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Matches 74; Conserv
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PROSITE: PSOUTE: AA.TRNA_LIGASE I: 1.
Ambhoacyl-trna synthetase; Protein blosynthesis; Lidase; AIP binding.
"HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                                    000754; 093094; 016680; 015330; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) 10-Rel 19-Last annotation update) 12-Rel 19-Last annotation update) 12-Rel 19-Last annotation update) 12-Rel 19-Last annotation update) (MANNOSIDASE PRETURSOR (EC 3.2.1.24) (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN).
                                                                                                                                                                        mannosidase cDNA and identification of siblings.":
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Mammalia: Entheria: Primates; Catarrhini; Hominidae; Homo.
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                  (MANH)."
                                                       Riise H.M.E., Berg I.,
Peccherini I.,
                                                                                           MEDITINE
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                Hum. Mol. Genet. 6:717
                                                                                                                                                                     Staticas
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"Alpha-mannosidosis: functional cloning of the lysosomol alpha
                                                                                                                                                                                                                                                                MEDILINE:
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                                  "Genomic structure of the human lysosomal alpha mannosidase gen
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42:200-207(1997).
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                                                                    Nilssen O., Romeo G., Tollersind O.K
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rartial sequence of the purified protein confirms the identity of cDNA coding for human lysosomal alpha-mannosidase B."; Hiochem. J. 305:363-366(1995).
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                                                                                                      modified and this st
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                                                                        or send an email to licensedisb-sib.ch).
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                            EMBL
                                                      EMBL: U60266; AAC34130.1;
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                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Spectrum of mutations in alpha-mannosidosis.";
Am. J. Hum. Genet. 64:77-88(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lollersrud O.K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liao Y
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CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON ALPHA-D-MANNOSE RESIDUES IN ALPHA-D-MANNOSIDES. SUBCELLULAR LOCATION: LYSOSOMAL.
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               U60885;
U60886;
                                            U60899;
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                                                                                                                                                                                          /FTId-VAR_003338
                                       -> P (IN AM)
                                                                                                                                    -> P (IN AM)
                                                                      -> R (IN AM)
> H (IN REF. 3).
11425F6A340F33E1 (RC64;
                                                                                                                     (IN AM;
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                                                                                                                                                                                                                                                                                    (GLCNAC
                                                                                                                                                                                                                                                                                             ALPHA-MANNOSIDASE D PEPTIDE
                                                                                                                                                                                                                                                                                                             ALPHA-MANNOSIDASE A
ALPHA-MANNOSIDASE B
ALPHA-MANNOSIDASE C
                                                               _003346
                                                                                                                                                                                                                                                                                                                                    ALPHA - MANNOS I DASE
                                                                                                                     RAPE
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                                                                                             Matches
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Best Local Similarity
148 - NVLRRQIINPKG----
                                                              9
                              ARGCLDSAGPWIMS-----RALRPPLPPL--CFFLLLLAAAGARAGGYEICPTVQPNMLN 63
                                                           ARHGRDQDGNWYFALDQEGKPLRQPYNVFSDCFAAMAFSQY-ALASGAQEAKATALQAYN 147
                                                                                          4.4%;
ilarity 17.7%;
Conservative 4
-QY-----EKSYPGTRPLKSLAVPMILANLT----
                                                                                           46;
                                                                                                        Score 94.5;
Pred. No. 4
                                                                                           Mismatches 134;
                                                                                                                         13B 1 :
                                                                                                                       Length 1010;
                                                                                          151:
                                                                                       Gaps
                                                                                           17;
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SEQUENCE

2443

CATALYTH

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01 FEB 1996 (Rel. 43, Last sequence update)
01 of 1996 (Rel. 44, Last annotation update)
ALENYLATE CYCLASE (FC 4.6.1.1) (AFF PYROPHOSPHAIE-LYASE) (ADENYLYL CYCLASE).
                                                          NIVW
                                                                                                                                                                                                              was by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and to
                                                                                                                                                                                                                                                         This SWISS PROLEUTTY is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics, and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                               Grines 1997, 8:2805-2815(1994).
FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                              maydis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Pungi; Bas
Ostilaginomycetidae;
                                                                          Lyase
                                                                                         PHAM: PEGGSEG: LRR; IS
                                                                                                                                                                                                 entities requires a license agreement (see http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SERVIENCE EROM N.A.
                                                                                                                                                                                                                                            the European Biointormatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gold S., Duncan G., Barrett K., Kronstad J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDITINE: 82081885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ustilago maydis (Smort fungus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYAA HSIMA
P49686;
                                                                                                                        INTERPRET TERROOTS (C)
                                                                                                                                     INTERPRO: IPROOLETT;
                                                                                                                                                                                  or send an email to licensesish sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "cAMP regulates morphogenesis in the tungal pathogen Ustilago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DACT OF REMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 DYFINVATAÇGRYYKTNHTVMTMGSBEÇYENANMWEKNIDKITRIVNAÇÇAKGSSVHVIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .7
                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                                                                                                       MANY PROTEINS
                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                       SIMILARITY: RELONGS TO ADENYLYL CYCLASE CLASS 3 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHILLEBEHDOVGWEKTVDQYFYGEKNDEGHAGVQYEGSVESALLADPTRKFTYVETAFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEACYLWELNKANLIWSVKHOLETPYADGDHQFWTGYFSSK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NICTEPRYAMHTDEFCHSREQASLEAGMOFDGFFF
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                                                                                                                                                       [1349]B; AAA5/469.1;
                                                                         ka-parat ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCWQWFERVHDYAWS - - - - - HFADPEYGEWFGYLNRR 357
 17.7.1
17.1.1
8.1.3.1
                                                                       Leucine repeat; cAMP synthesis; Magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                    THE REPEATED LEGGINE RICH (LRR) SEGMENT IS FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rasidiomyceta: Ustiladinomycetes;
ae: Ustiladinales: Ustiladinaceae: Ustilado
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5941
7151
768
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POLY ALA.
PP2C LIKE
                                         POLY ASP.
                              LEUCINE RICH REPEAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI KAMMEMMDI AÇESGDEÇI, ÇEÇA LAVVI.NTI.E
                                                                                                                                                                                                                                                                                                                                                                       CYCLIC AMP + PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2493
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                                                                                                                                                                                                              Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                     SECOND MESSENGER,
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HCYB_PANIN
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Hest Local Similarity 22.6
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P10787;
01.JUL 1989 (Rel. 11, Created)
01.JUL 1989 (Rel. 11, Last sequence update)
30 MAY 2000 (Rel. 39, Last annotation update)
HLMGCYANIN B CHAIN.
                                                                                                                                                          interruptus refined at 3.2 A resolution
J. Mol. Biol. 209:249-279(1989).
-!- FUNCTION: HEMOCYANIN AKE COPPER-CON
                                                                                                                                                                                                                                                                                                                                                                                                                                  b and anomalous behaviour of subunits a and b on polyacrylamide geleetrophoresis in the presence of SDS.";
Eur. J. Blochem. 178:403-412(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HINAG HADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2152
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                                                                                                                                                                                                                                                                                                                                                                           X-KAY CRYSTALLOGRAPHY (3.2 ANGSTROMS)
Gaykema W.P.J., Hol W.G.J., Verei)ken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eumalacostiaca; Eucarida; Decapoda; Pleocyemata; Palinura;
Palinuroidea; Palinuridae; Panulirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Panulirus interruptus (California spiny lobster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1441
                                                                                                                                                                                                                                                    MEDIJINE: 90064489.
                                                                                                                                                                                                                                                                                                                      "3.2 A structure of the copper containing, oxygen carrying protein Banufirus interruptus hacmoeyanin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jekel P.A., Bak H.J., Soeter N.M., Verejken J.M., Beintema J.J.;
"Panulirus interruptus hemoeyanin. The amino acid sequence of subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJINE: 89091175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE
                                                                                                                                                                                                  "Crystal structure of hexameric hacmocyanin from Panulirus interruntus retined at 3.2 A resolution.":
                                                                                                                                                                                                                                   Volbeda A., Hol W.G.J.;
                                                                                                                                                                                                                                                                                                           Nature 309:23 29(1984)
                                                                                                                                                                                                                                                                                                                                                                Beintema J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STOS DAFMASE
                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 GKPLKQPYNVESDCFAAMAFSQYALASGAQEAKATALQAYNNVLKRQHNPKGGYEKSYPG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 KFV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Œ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 QVEDTOKFIWLONROVWOFAVFYNRLEPKPQWLEIAR
                                               AND C HAVE BEEN IDENTIFIED. SUBCELLULAR LOCATION: EXTRACELLULAR TISSUE SPECIFICITY: HEMOLYMPH.
                                                                                                                                                          FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
                            MISCELLANEOUS: THE B CHAIN CONTAINS TWO COPPER BINDING SITES
                                                                                                     SUBUNIT: HEXAMER OF A NUMBER OF DIFFERENT CHAINS, OF
                                                                                                                                         OF CURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS
             THREE HISTIDINE RESIDUES ARE LIGANDS TO EACH COPPER TON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPTGOVALVETD - TKNSTSLWETNNGMO - - - - TAMBEHNYLLEROLET FGSYEVKTEG 2104
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2493 AA; 271979 MW; 106A872030105HPB CR064;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94.5;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657 AA
                                                                                                                                                                                                                                                                                                                                                                               J.M., Soeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1: Length 2493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
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                                                                                                       WHITHM,
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SUBFAMILY

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mat ches
                                                                                                                                                               01-ABG-1992 (Rel. 24, Created)
01-ABG-1992 (Rel. 24, Last segmence update)
01-JHN-1994 (Rel. 29, Last annotation update)
ENDOSLUCANASE C PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE)
(CELLULASE) (EBC) (CELLODEXTRINASE C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM: PF00372; hemoryanin; 1.
PKINIS; PR00187; HAEMMCYANIN.
PR0SITE; PS00209; HEMORYANIN_1; 1.
PR0SITE; PS00210; HEMORYANIN_2; 1.
PR0SITE; PS00210; HEMORYANIN_2; 1.
PR0SITE; PS00498; FYROSINASE_2; 1.
Respiratory protein; Oxygen transport; Copper; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
VARIANT
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INTERPRO: IPRODUZZZZ
MEDILINE
                  SIRAIN-SP. CELLILOSA;
                                            SECHENCE FROM N.A.,
                                                                                 Pseudomonas
                                                                                                          Hacteria: Proteobacteria;
                                                                                                                             Pseudomonas thuorescens
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HSSP; P04254; 1HCY
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                                         AND SEQUENCE OF 38
                                                                                                          gamma
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COPPER A.
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Pred. No. 4.2;
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PEAM: PE00150: cellulase: 1.
PEAM: PE00561: CHD_BACLERIAL: 1.
PROSITE: PS00561: CHD_BACLERIAL: 1.
PROSITE: PS00659: GLYCUSYL_HYDROL_F5: 1.
Cellulose degradation: Hydrolase: Glycus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               consists of multiple functional domains.";
Biochem. J. 279:793-799(1991).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1.4 BETA D-GLUCOSILIC LINKAGES IN CELLULOSE.
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INTERPRO:
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5; Mismatches 111;
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01 NOV 1995 (Rel. 32, Last Sequence update)
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1SoleHeVL TRNA SYNTHETASE (BC 6.1.1.5) (ISOLEHCINE
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FORTALYHIC ACTIVITY: ATP + L ISOLEHICINE + IRNA(ILE)
FYROCHOSPHATE + L ISOLEHICYL TRNA(ILE).
FORTALYHOR: HINDS ONE ZINC ION (BY SIMILARITY).
F. SHRUNTI: MONOMER (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brown J.R., Doolittle W.F.;
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democyanin a chain.
                                                                 PIR; A24183; BHLOA.
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Structure of panalitus interruptus hemocyanin and evolution of
arthropod hemocyanin, pp.33-62, brukkeri) Van Benderen,
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                                    P 35.
                                                                                                                                                                                                                                                                            interruptus retined at 3.2.A resolution."
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"Crystal Structure of hexameric haemocyanin from Panulirus
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Gaykema W.P.J., Hol W.G.J., Verei)ken
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Eakaryota: Metazoa: Arthropoda; Crustacea: Malacostraca:
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                                                                                             MISCELLANDOUS: THE A CHAIN CONTAINS TWO COPPER BINDING STREEF HISTIDINE RESIDUES ARE LIGANDS TO EACH CORPER TON. SIMILARITY: BELOWES TO THE TYROSINASE FAMILY, HEMOTYANIN
                                                                                                                                                                                                                                             MOL. BIOL. 209:249-279(1989).
FUNCTION: HEMOTYANIN ARE COPPER-CONTAINING OXYGEN CARKIERS
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SUMMARIES

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Matches 140; Conserv
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Submitted (MAK 1995) to the EMMI-ZenHank/DBG databases.

I. FUNCTION: CATALYZES THE INTERCONVERSION OF N ACCIVING CONCERN CONCER
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Of MAY 2000 (Trematrel, 14, Last sequence update)
Of JUN 2000 (Trematrel, 14, Last sequence update)
N ACTIGUTOSAMINE 2 EPIMERASE (EV 5.1.3.8) (GLCNAC 2 EPIMERASE)
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CATALYTIC ACTIVITY: N ACETYL D GLUCOSAMINE - N:ACETYL D
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Pred. No. 8.5e 49;
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P74606;
01-FEB-1997 (TrEMRLIPEL 02, Created)
01-FEB-1997 (TrEMRLIPEL 02, Last sequence up
01-JUN-2000 (TrEMBLIPEL 14, Last annotation
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                                                                                                                                                                                    026180)
01-N.V.1996 (TrEMBLPEL 01, Created)
01-N.V.1996 (TrEMBLPEL 01, Last sequence update)
01-MAY-2000 (TrEMBLPEL 13, Last annotation update)
HEMOCYANIN PRECURSOR [CONTAINS: HEMOCYANIN, LONG FORM; HEMOCYANIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the genome of the unicellular cyanobacterium Synochocystis sp. strain PCC6803. II. Sequence determination of the entire denome and assimument of potential protein-coding regions.";
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                                                       Penaeus vannamei (Penoeid shrimp) (European white shrimp).
Eukaryota; Metazoa; Arthropoda; Ernstacea; Malacostraca;
Eumalacostraca; Eurarida; Decapoda; Dendrobtanchiata; Pendeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein
SEQUENCE 607 AA;
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                                                                                                                                                             SHOKE FORM .
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Pred. No. 0.42;
47; Mismatches 1
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Best Local :
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INTERPRO;
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PROPEP
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FEBS Lett. 407:154-158(1997)
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Sellos D.Y., Lemoine S., Van Wormboudt A.;
"Molecular cloning of hemocyanin cDNA from Penaeus
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PROSITE: -S00498: TYROSINASE_2: 1.
Signal: Respiratory protein: Oxygen transport: Copper
Endoplasmic reflection: Metal-binding.
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PROSITE: PSOO209; HEMOCYANIN_1;
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PQ4254; IBC1.
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IPR002227;
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74980 MW;
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22.5%; Pred. No.
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COUPPER A (BY SIMILARITY)
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Best Local Similarity
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AMTSED
                                            "Skibbiga M., Zhane H., Endo A., Skishikura K., Kushiro I., Ebizuka Y., "Two branches of the hipped segritase gene in the molecular evolution of plant oxida eparateur cyclases."

Eur. J. Kreebem. 2003 802 807 (1999).
                                                                                                                                                                                                                                                             Of MAY 2000 (TERMIGRAL, 13, Created)
Of MAY 2000 (TERMIGRAL, 14, Last Sequence update)
Of JUN 2000 (TERMIGRAL, 14, Last annotation update)
LUPEGI SYNTHASE (EC. 5.4.99.).
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Bukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
Memoliophyta: endicotyledons: Rosidae: enrosids II: Brassicales:
              EMBL: AB025443; BAAR6440.1;
INTERPRO: IPRO:11440;
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                                                                                                                                                                                                                            olea europaea (Common olive)
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Walker M., Brooks S., Altali H., Araujo R., Conn L., Conway
Conzelez A., Bansen N.F., Huizar L., Kremenetskaja I., Lenz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN 2000) to the EMBL/SenBank/DDBJ databases. EMBL: ACO07544: AAF24535.1;
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Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
"Genomic sequence for Arabidopsis thaliana BAC F7F22 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F/F22.5
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                                                                                                                       TESSUE LEAF:
                                                                                                                                       SECUENCE FROM N.A.
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20.3%; Pred. No. 1.2;
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Best Local S
Matches 61
                                                                                   Wilson K., Ainscough K., Anderson K., Haynes C., Herks M., Bontield J., Burton J., Connell M., Copsey L., Cooper J., Confson A. Craxton M., Dear S., Du Z., Durbin R., Favello A., Fullou L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister L., Lightning H., C'Callaghan M., Farsons J., Fercy C., Kifken L., Roopia A., Saniders D., Shownkeen F. Smalden N., Smith A., Sounhammer E., Staden K., Shiston J., Thomas K., Vaudin M., Vandhan K., Waterston K., Waterson A., Weinstock L., Wilkinson Spread J., Wohldman P.; W. M. Contiguous nucleotide sequence from Chromosome III of C.
            PEAM: PEOUO48: SST:
                                                                                                                                                                                                                                                                                                                                                                                                       Caemorhabditis elegans
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                                           Nature 368:32:38(1994).
EMBL: 793377; (AB07572.1; -.
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758 AA:
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29470 MW;
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Last aumotation update)
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45EF8EC8EDBAE912 CRC64;
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Matches 56
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Best Local Similarity
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PEAM: PF00134: URNA-SYNTHILE:
PRINTS: PR00984: TRNASYNTHILE:
PF0SITE: PR00178: AA, TRNA_LIGASE_I: 1.
Amitroacyl-trna synthetase:
SEQUIENCE: 1067 AA: 126108 MW; H7A8C
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL: AJ248285; CAB49833.1; -.
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INTERPRO; IPRO02300;
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                             _cGHPPQOLEWDCKLWWVH---LETLVALAKG----HcATGOEKGWOWFEKVHDYAWSHFA_343
                                                               EFKGREL - LGLRYVHILMD-
                                                                                           STEGREENPGHG LEAMWEMMDTAQRSGDRQEQATAVVENTEEYAWDEEFGGTFYFLDR
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                                                                                                                                                                                                                                                       56.;
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56: Conservative
PROKEFKEKYEWAHRVILADEVILEEGTGLVHTAPGHGE--
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20.4%;
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                                                                                                                                                                                                                                                   24; Miss Tobes 47;
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             Q9ZVW2:
01-MAY-1999 (TEEMBLEEL 10, C
01-MAY-1999 (TEEMBLEEL 10, L
01-JUN-2000 (TEEMBLEEL 14, L
14E14.10 PROTEIN.
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Deckett G., Walten P.V., Gaasterland L., Young W.E., Lebox A.L.,
Graham D.E., Overbeck E., Snead M.A., Keller M., Aujay M., Hober
Feldman R.A., Short J.M., Olson G.J., Swam b K.V.;
"The complete genome of the hyperthermophilic bacterium Aquitex
apolicus.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               057902;
01-AUG-1998 (TrEMBLiel, 07, Created)
01-AUG-1998 (TrEMBLiel, 07, Cast sequence update)
01-AUY-2000 (TrEMBLiel, 13, Last aunotation update)
HYPOTHETICAL 80.9 KDA PROTEIN.
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EMRL: AE000775: AAC07873.1; -.
INTERPRO: ITERCOUR 44: -.
PROSITE: PS00123: CARBOXYPEFT_ZN_2: UNKNOWN_1.
Hypothetical protein.
SEQUENCE 692 AA: 80864 MM: 17CB4CDDAB97235
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Bacteria: Aguiticales:
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Arabidopsis thaliana (Mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                              692 AA; 80864 MW; 17CB4CDDAB972354 CRC64;
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                                                                                                               PRELIMINARY:
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Last annotation update)
                                                                            Created)
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Query Match
Test Local Similarity
Matches 40; Conserv
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Best Local Similarity
Matches 60; Conserv
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098W42;
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of MAY 2000 (TrEMHERE). 14, Last sequence update)
of JUN 2000 (TrEMHERE). 14, Last annotation update)
flyporHETICAL 44.5 KDA PROTEIN.
THILLITO.
Authorist thatiana (Monse car cress).
Authorist Viridiplantacy Emblyophyra; Frachcophyta;
Enkargolophyta; endicotylodons; Rosidae; enrosids 11;
                                                                                                                                                                                                                                      Vos P., M
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EMBG, ACOUSTI: AACC/203.1;
INTERPRO: IPRO01410; -.
                                                                                                                                         SEQUENCE From N.A.

EXTAGABLICASES sequencing project;
Submitted (JUNE 1993) to the EMBL/GenBank/DDBJ databases
EMBL: ALO79447: CAB45454.1;
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                                                                               SEQUENCE 391 AA;
                                                                                                          ENTERPRO: TPROBOGOS; PIPLO X DOMAIN; L.
                                                                                                                                                                                                                                                                                               Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                      Submitted (JUN 1999)
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Mewes H.W., Mayer K.E.X., Lemeke K., S
ed (JUN 1999) to the EMBL/GenBank/DDBJ
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24.0%;
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 Pred. No. 7;
3; Mismatches
                                Score 91;
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                                Length 391;
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 Indels
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Brassicales;
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Best Local Similarity
Matches 49; Conserv
01 NoV : 1999
01 NoV - 1999
01 MAY - 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1999) to the EMBL/GenHank/DDBJ databases EMBL: AF169229; AAL49730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and expression of chrysoptin, a salivary gland protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tahanomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                              Signal
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INTERPRO; IPR002224; -.
PF01009; 5_nucleotidase; 1.
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Leiner E.A., Reddy V.B.,
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                                                                                                              MKAWOEFVHEKGOEVVAESPVVLSKENCRVSIKINIGNEFTDAYVHEYVSSH
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554 AA;
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Pred. No. 14
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                                                                                                                                                                                                                Merson Davies L.A., Condille E.;
"Analysis of live tylosin biosynthetic genes from the
the Streptomyces fradiac genome.";
Mol. Microbiol. 18:349-355(1994);
-!- SIMILARITY: HELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. SIRAIN-159235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TEMBLIEL 01, Created)
01-NOV-1996 (TEMBLIEL 01, Last sequence update)
01-MAY-2000 (FEMBLIEL 13, Last annotation update)
CYTOCHROME P450 (EC 1.14.14.1).
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FEASITE: FSOOLOS; FEATEL KINASE_ATE: FSOSLE: PSOOLOS; PROTEIN_KINASE_DOM: FKOSLIE: PSOOLOS; PROTEIN_KINASE_DOM:
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PROSTIE: PS00086; CYTOCHROME.P450; UNKNOWN I.
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HEME (BY SIMILARITY).
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Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	* Query Match Length DB ID	Ť	11)	Description
- :	1173	100.0	128598	2	2 D96912	190912 Synechocyst
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proteins with reference to the function of the Leucine zipper motif
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Eutheria: Rodentia; Seinroquathi; Muridae; Murinae; Rattus.
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Levelue Alpper; remin; remin-binding protein.
Homo sapiens (strain:Caucasian) 3-month old male Wilms' tumo:
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hepailment of Biochemistry
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proteins with reference to the function of the leucine zipper model. J. Biochem. 110 (4), 493-500 (1991)
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Entheria: Primates: Catarrhini: Hominidae: Homo.
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Homo sapiens
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/cell_type-"Wilms, tumor"
/celone-"lambda HRH6"
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Patent: US 5795767-A 5 18-AUG-1998; l (bases 1 to 1209) Isukada.Y., Ohta,Y. and Maru,I. KEYW FUS VERSIEN VOLESSION DEFINITION SEST AROZ4DO3 大学のコー

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Molecular cloning and identification of Nacyl-D-glucosamine
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Submitted (04 MAK 1996) to the DBBJ/EMBBJ/GenHank databases.
Maru, Marukin Shoyu Co., Ltd., Kyolo Kescarch Laboratories:
Mentomae, Teato, Uji, Kyolo 511, Japan
(E mail:LDV05011=miltyserve.or.)p, Tel://4 22 0941,
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/clone="pEPIl"
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/product "adremoleukodystrophy protein" /evidence-experimental /evidence-experimental join(<4746, .4886,4969, .51<7.6583, .6647,9754, .9899, 10207, .10352,12535, .12619,12848, .12974,14057, .13276) /dene-"Aldgh" /note-"adremoleukodystrophy protein /dec.no. 234637	/evidence-not_experimental join(4744, 4886,4969, 517,6554, 6647,9754, 19899, 10207, 10352,12535, 12619,12848, 12974,14057, 14274) /deme-"Aldyh" /note "adrenoleukodystrophy protein /acc.no. 244647"	/rpt_lamily~"(cXTA)n" -widence-not_experimental complement (44314577) /rpt_family~"LIMB7"	complement(41984287) /rpt_family_"pB[D7" /ryidence-not_experimental 43124366	/	/rpt_tamily-"82" /evidence-not_experimental complement(3635, 4018) /rbt_family-"i_MM7"	/rpt_tamily-"82" /#vidence-not_experimental complement(33833519)	Complement (3.24]	/evidence-not_experimental complement(3147, 3214) /rpt_family="PBHD9" /ruidanarana	/evidence-not_experimental complement (2970, 3090) /ret_lamily="Bl_MM"	— a.ı	/rpt_tamily="PHID/" /Pvidence-not_experimental complement(25662710) /rpt_tamily="RSINE]"		complement (18912207) /rpt_tamily="LIMA4" /evidence-not_experimental complement (22472382)	/evidence-not_experimental complement(16421789) /rpt_tamily-"Blamm" /evidence-not_experimental	/rpi_tamily="LIMB7" /ryidence=not_experimental complement(1581. 16 49) /rpt_family="polypurine"	complement (865.7.1063)	/ Yeldone - not_experimental complement(702864) /rol_lamity="134" /widene.rot_extractmental	Atot tamily "GAAAAYD"

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    arbitrary, daps between the confids are represented as
    runs of N, but the exact sizes of the daps are unknown.
    This record will be updated with the finished sequence

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                                                                                                                                                                                                                                                                                                                                                                   64645 64744; gap of 100 bp
64745 65998; contig of 1284 bp in length
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76482 77816; contid of 1035 bp in length
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72028 74077: conf
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56309 58154: contin of 1845 bp in length
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53651 56208; contid of 2558 bp in length
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41983 43169: contiq of 1187 bp in length
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39681 41882; contig of 2202 bp in length
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35416 37447; contig of 2032 bp in length
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28659 34103: confid of 5445 bp in Tength
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16423 17987; contig of 1535 bp in length
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4676 7454; contid of 2679 bp in length
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61087: contin of 1027 bp in length
               85114: gap of
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85014: contig of 1911 bp in length
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39580: con
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51711: contig of 1456 bp in length
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10650: contid of 1830 bp in length
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2409. _4575
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                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                               /clone_lib-"RPCI-11.1"
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97063: contig of 1166 bp in
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                                       * consists of 40 contigs. The true order of the pieces is is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are anknown. * This record will be updated with the Linished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                     Insert size: 150212; sum-of-contigs
Insert size: 159639; agarose-fp
Quality coverage: 2.85% in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                             Consensus quality: 13270 bases at least Q40 Consensus quality: 13270 bases at least Q40 Consensus quality: 138219 bases at least Q30 Consensus quality: 142824 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-JUN-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                        * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humguery sanger.ac.uk
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1 (bases 1 to 154112)
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                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently
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Matches 71; Conserv
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intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence comparison of the Caenorhabditis elegans dpy-13 and col-34 genes, and their deduced collagen products Gene 120, 261-266 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cox,G.N., Fields,C.A., Kramer,J.M., Rosenzweig,H. and Hirsh,D. Sequence comparisons of developmentally regulated collagen genes of Caenorhabdilis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93013043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89326131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 76, 331-344 (1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen
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99558, 102566
                                                                                                                                                         /codon_start=1
/product="alpha-colladen"
/protein_id="AAA27985.1"
/db_xre1-"G:156250"
/translation="MOLETRIKAYRFVAYSAVAFSVVAVISVGVTLPMVYNYVHHVKR
                                                                                                                                                                                                                                                                                                 /genc="alpha-collagen"
foin(585. .665,720. .1362,1411. .1583)
/gene="alpha-collagen"
foin(585. .655,720. .1352,1411. .1583)
/gene="alpha-collagen"
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97110. .99457
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102667. .109303
                                                 PPGDSGEPGSPGLPGGDAAFGEPGPKGPKGPBGAPGAFEHGESQECPRGEPLLPGEPG
PPGEAGPQGPPGSPGQPGAFGSPGQPGPKGPNGPDGQPGAFGPAGPAGPPGSPGF
                                                                                                           GPPGPAGTPGKPGRPGKPGAPGLPGNPGRPPQQPCEP1TPPPWKPCP0GPPGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xre1="taxon:6239"
381. .393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Caenorhabditis elegans"
/strain="N2"
                          RGICPKYCAIDGGVFFEDGTRR"
                                                                                                                                  TMHNEITECKGSAKDIWNEVHALKSLPNSNRTARQAYNDAAVTGGGAQSGSCESCCLP
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57.78;
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Best Local Similarity 49.3%;
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                                                                                   Miller, N and Bradshaw, H.

The sequence of C. elegans cosmid F36A4
Unpublished (1996)
3 (bases 1 to 42936)
                                                                                                                                                                                                                                                                                                         Latrellle, P., Lidhthing, J., Lloyd, C., McMurray, A., Morrimore, B., O'Calladhan, M., Parsons, J., Percy, C., Kilken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sourhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaddin, M., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaddin, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans cosmid F36A4.
U53333
                   Direct Submission
Submitted (01-APR-1996) Robert Waterston
                                                              Waterston, R.
                                                                                                                                                                                                                                                 Wilkinson-Sproat, J. and Wohldman, P. 2.2 Mb of contiquous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                   Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
                                                                                                                                                                                                                                                                                                                                                                                             Fulton,L., Gaidner,A., Green,P., Hawkins,T., Hillier,L.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J., Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans strain-Bristol N2.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U53333.1 GI:1255801
                                                                                                                                                                                                          Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                               elegans
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                                                                               (bases 1 to 42936)
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/qene-"alpha-collagen'
a 551 c 534 q
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720. .136
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1363...1410
/gene-malpha-collagenm
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Submitted by:
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Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Auderson, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baynes, C., Berks, M.
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the program Genetinder(P. Green and L. Hillier, ms in preparation)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osmid is E3085, 200 by eventap; \ell' cosmid is E15E6. this cosmid is at base position 197 of CELE36A4.
                                                                                                                                                                                                                                                                        / Reso "sums 1"
| bring 9528 | 19611, 9682 | 19771, 9869 | 110197, 10682 | 111490 |
| 11719 | 116244, 12331 | 113111, 13410 | 113853, 14214 | 114954
| 15409 | 116997, 17400 | 17507, 18028 | 18213, 19021 | 15122)
| Zdeno "sums 1"
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/db_xrot_"G1:1255862"
/toanslation="MOLETICIKAYREVAYSAVAESVVAVISVCVTLEMVYNYVHHVKR
/product "C. elegans DNA directed RNA polymerase II large subun)t (ama I) (SP:Pl6(56)"
                                                                                     ykhakobis; coded for by C. elegans cDNA ykłaczis; coded for
by C. elegans cDNA ykłaczis; coded for by C. elegans cDNA
ykłacilis, coded for by C. elegans cDNA ykłaczis; coded
for by C. elegans cDNA ykłatzis; E46A4./*
                                                                                                                                                                                                            Zhote "coded for by C_{\infty} elegans cDNA yk4 all.3; coded for by C_{\infty} elegans cDNA yk84f7.3; coded for by C_{\infty} elegans cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKEST LIPDDY LIWCYSENKNYDIG LLNLANKY IGI FILETLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAA96157.1"
/db_xret="GI:1255804"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVWKLESPIGPACTIPGATSWONLVHNDLONHKETEPRPLASSEAFGEPATPEDSISGE
PRSODM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence-not_experimental
/protein_id "AAA96156.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note "weak similarity to collagen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(6296, .6471,6810, .6960))
/deno="F36A4.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(6296, .6960)
/deno="E36A4.11"
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PEĞDEĞĞERĞERĞLEĞQDAAIMERGEREKĞERPIQERĞARĞARĞLEÇÇEÇEÇEVLEÇEPLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(4926, .5098,5147, .5792,5847,
/qene "F36A4.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (4926, 15927)
Zarne "F36A4, 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start-l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     )oin(8261. .8429,8478.
/dono:"F36A4.8"
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/translation="MedickowKenVheelkKTVTGRSTGFGYVRGSWEEEYELKNEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zeodon start 1
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/dbromosome="IV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism "Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                               Zoodon start 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cambridge CHIO IRD, England e mail: tw/hemalode.wustl.edu_and_jes/sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEIGHBORING COSMID INFORMATION:
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bepartment of Genetics, Washington University,
St. Louis, Mo. 63110, USA, and
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KQAQYNATITMATITKSTIGTKNMCTKSKLNSEAFI-MITGEFESKEGQATAGJEGEMVG
ALAAQSIGEPATOMIT.NIFHYAGVSAKNVITGVPRIKELINVSKILKTISITVELIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation "MEALDSSSETFF@DYEESYVVNHN°SADONIYCV@PVKFFIVSK
FGTRVIKFDIKALPVGSPIFCKSPKEWRVIKG"
28971.__29539
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FECKECEEGEAGPEGEEGIEGIAGINGTNAAFGAEGENAFEGEAGEGFEGEEGGEGGEGAEG
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/dene-"F46A4.4"
                                                      KUHKEVDIJERPKTYYENTEARPNAUPYKCKAPWIF" <1074. 141526
                                                                                                                                                                        DVTVHDLLKQDKF0TSERTKTVKYTTDAEDDFPTDNFFTFYKFNHN0SANGKTY0VKF
                                                                                                                                                                                                                  /translation "MHLPTFCLVTL/SLISCTHTRF@AETDCDTPGAYWCGELNVLEK
                                                                                                                                                                                                                                                                              /evidence not_experimental
/protein id="AAA96161.1"
/db_xret="G1:1255808"
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/protein_id "AAA96160.1"
/db_xtet-"G1:1255807"
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join(27626, .27765,27812, .27902)
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/protein_id-"AAA96159.1"
/db_xret-"GL:1255806"
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/codon_start |
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EQQTTDEDTIVIGMBEQFARPEWMTCTVLPVPPLAVRPAVVTF3SAKNQDDLTHKLSD
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/db_xref-"G1:1255805"
/translation="MALVGVDEQAPLKIVSKVQEGILGFEELKKMSVAHVEEFEVYEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5020 CCGGACCACCAGGAICCCCAGGAGA 4996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5140 AAAGATGITAIAGGTGACCIAITTTTAAAACTTGICTTTCAGGACAACCCGGACCAAAGG 5081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        952 ggreaceaugeeact ggeeaagaaa 976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctygaatqqqaccaaaqctctqqtqqttqccaaq 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101;
                                                                                                                                                 Direct Submission
Submitted (27-APR-1998) Nematode Sequencing Project, Sanger Centre, Submitted (27-APR-1998) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, Endland and Department of Genetics, Washington University, St. Louis, Mo 63110, USA, E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
Enkaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Khabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                      jes sanger.ac.uk or rwanematode.wustl.edu
en Sep 22, 1998 this sequence version replaced gi:3093277.
Coding sequences below are predicted from computer analysis, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erratum:[[published errata appear in Science 1999 Jan
1:283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep
3:285(5433):1493}]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans cosmid C24F3, complete sequence AL022716
predictions from Genetinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                            McMurray, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The C.elegans Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81969066
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                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 14544)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence-not_experimental
/protein_id-"AAA96163.1"
/db_xref-"G1:1255810"
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/protein_id="AAA95162.1"
/db_xre1="GI:1255809"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKVHKWVGHRRVKFLIDASANGKPKTCEWPFFYGGFWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(32592. .32728,32795. .32885,32932. .33126)
/dene-"F36A4.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /qene="F36A4.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPHCKPSRCKPPFYF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(31073, .31155,31211, .31304,31350, .31526)
/qene="F36A4.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start-l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MFEAEID?NIPGALWCGELYVLEQDVVFPDLLRIDRFCTSKSKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14544 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 33126
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0: Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 42936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOULCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             left end of clone F01G10 is at 14441 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence AL021570. The end of this sequence (14441. .14544) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neighbouring submissions. The true left end of clone 0.24F3 is at 1 in this sequence. The true
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overlapping sections once, or longer because we arrange for a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bin/display?db-wormacc&class-Sequence &object-02483
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overlap between neighbouring submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the specified clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unambiquously on both strands, or on a single strand with both a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      It may be shorter because we only sequence overlapping sections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPORTANT: This sequence is not the entire insert of clone C24F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                         GDGTLESSDNVRTGFETGEELWSARSTNVRLAÐUGVDTMCNGSGSHHTLGKSNYRTNU
LILGSSAKVGGVYLYANORGCDGDKVYYDGASSVAONGDLLAGTHOFDTEDTSVVSAV
VDLSDNOCFRHKKSSDKGNASDOVTVVPTRFDGKMTGGTKYNEKSTAPTHNVEDLGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"mnowdrrckvalctvnnwaldekgnyeklvklceeaaaldakik
LGPELEIPGYGCADHEFELDTERHSWEMLSKLVEKSKKWPNLLVVTGLFTKERGLLYN
CAAALENGKLLFIRAKWGLADDNVYRESKWFVKWTETTKHYJWELNSDIHFJJETVFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA EST yk641
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(3350...3553,3600...4079,4128...4203,
4336...4433,5787...5857,5907...6021,6071...6159,6204.
6420...6764,6810...6945,6997...7231,7487...7580))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(3350. .3553,3600. .4079,4128. .4203,4336. .4433,5787. .5857,5907. .6021,6071. .6159,6204.6420. .6764,6810. .6945,6997. .7231,7487. .7580))
                                                                                                                                                                                                                                                                                        GIFIDTIVTSILKVENVAYGEMPSFQSPDNRETMALONIQARIKMVLSYLFAQLALVS
HKRPGGLLVLGTANVDESLVGYLTKYDOSSADINPIGSVSKKDLRQFLEIAYEKYGMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA EST yk362d4.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUNA
similar to CUITCLE COLLAGEN 1
                                                                                                                                                                                                                                                                ALRGV1DS)PTAELKPLVDGKVAOTDEAETGLTYDELSVTGKLRKPGGMGPYGMFLKI
                                                                                                                                                                                                                                                                                                                                                              TDGGDDDPAYYLGGKKVGEDPAELCNQVLFTCYMASEHSSDETRQCAEGLAKNVNSSHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id-"CAA18773.1"
/db_xref-"G1:3874484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome-"1
/clone-"C24F3"
                           /note-"predicted using genewise
                                                                 /qene-"C24F3.6"
                                                                                                                                                                                              DESYGEERTREKOVELKKNST"
                                                                                                                                                                                                                             LOLWODKYSIDELEEKVNKFFWRYRVNRHKATVSIPAIHAENYSPODHRNDHRPFLYP
                                                                                                                                                                                                                                                                                                                                                                                                PLAELCHGPPAYLWTYLRRSGMAGYFTPLSGGQDSSAVAAMVKLMCEKVCGATKRRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref≃"SPTREMBL:Q9XXK6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"cDNA EST CEESW54F comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /qene-"C24F3.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="C24F3.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_x1 ef = "taxon : 6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Caenorhabditis elegans'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                /qene-"C24F3.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      this sequence is NOT necessarily the entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .14544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST yk259h4.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST yk89h6.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST yk502q2.3 comes from this gene EST yk89h6.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yk641a2.5 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yk362d4.5 comes
yk502g2.5 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yk259h4.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yk641a2.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yk89h6.5 comes from this gene
                                                                                             .4834,4885.
                                                                                                                                                            .4834,4885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from this gene'
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cDNA EST yk92d4.5 comes from this

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ANG:
/Translation "MWKTLENLYLAQLEMIVGETSKGEESKNDIKRVLILITEPISEK
GKTGSVDYKFLHLLIMFDEFTLINATLETAVLYTNEGVEKEENVGVHGLAAVSKSVST
GAAYLMYKNUWPVEKALKMTESVPKETGPNAGFLAGLKTWEKSGMSESADQYKNLKTD
                                                                                                                                                                                                                                                    /protein id "MAAIK//L.L"
/db xref "GI:8874482"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA EST yk452e5. & comes from this dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similar to buil specificity phosphatase, catalytic domain clNA ESI yk 6d4.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhote "CDNA EST yklyde5.5 cames from 'Sis dene
cDNA EST yklyde5.5 cames from this dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhote "predicted using depetinder cONA EST ykSle5.5 comes from this gene CONA EST yk4 06-12.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA EST 9k452c5.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dette "02483.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STAYFENETRVALALL (LLEYTTOLL FELIAREAHEVGRKGLSDPAFKLENGSEVLYRL)
STAYMENVER GERVELLALL (LLEYTTOLL FELIAREAHEVGRKGLSDPAFKLENGSEVLYRL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILLESTATION - MAKEDOSKASKKPODELTSHEELTONEDDINGDEWAYPTOLESTAND FOR THE STATE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA18772.1"
/db_xref_"GI:3874483"
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                                                                                                                                                                                                                                                                                                                                                                                              Zeedon Start 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note "predicted using denetinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11600. (11799,11845. (11903)
Zaono "c2463.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )oin(la845,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KERESINAKKEKKKSAAAAAAVEKKEKKRQUSESUSKKKN*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VWIGYETEHRVMSAAYKLYETEQTSYWIHGEFEEYLGKLKROETROKSVQATLHTAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOEYGLDKISKKTHLSKVSTEKEGESENQMEETVYSIAHAFYIVSERLEDESEVKSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /done="024F3.1b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(8085, .8111,8261, .8882,8925, .9055,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESNAKKEKKKSAAAAAAVEKKEKKRUUSESUSKKKN"
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VILDISTATION TSKYTHISKVSTEXFOLDSFHJØMFFIVYSLANDEDELSFYSVOLWVETVIJM

ZD DISTATION "MYKPGGSKASKREGPFILSHEFILONBODIMSOVVMVFIVGIM

VJUDGIDK ISKKTHLSKVSTEXFOLDSFHJØMFFIVYSLANDLIJDELFYSVOLWVETVGIM

VJUDGIDK ISKKTHLSKVSTEXFOLDSFHJØMFFIVYSLANDLIJDELSFYSVOLWVETVGIM

VIDDOLIK SKKTHLSKVSTEXFOLDSFHJØMFFIVYSLANDLIJDELSFYSVOLW

VIDDOLIK SKKTHLSKVSTEXFOLDSFHJØMFFIVYSLANDLIJDELSKSTANDLIJDELSK

VIDDOLIK SKKTHLSKVSTEXFOLDSFHJØMFFIVYSLANDLIJDELSK

VIDDOLIK SKTHLSKVSTEXFOLDSFHJØMFFIVYSLANDLIJDELSK

VIDDOLIK SKTHLSKVSTEXFOLDSFHJØMFFIVYSLANDLIJDELSK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /domo "c24F3.la"
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9213. (9554))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /qone "c24F3.1b"
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CALLABYVFFEIMHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPPGPPGPEGPNGEFONKOPAGPPGPGKF\\DAGPPGENGNNGEPQPGAPGEPGQPGQ
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VMHSDTVETKSEAGKLESGVNKTEDLMMAHNKTARGAGEDNGGEGGTLEGAGGEGNKGEL
POSAGRERKEGARGLNGNEGREPKEEG EPLITPEEG KEGPEGFEGFEAGFEGDNKGEL
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/db_xref="d1:9367025"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(10845. .10931,10982. .11169,11215. .11328,11375. .11545,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zahi xiet "GI: 8874481"
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EST yk669a4.5 comes from this gene"
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             of Washington, Po Box 457730, Seattle, WA 98195.
* Note: This is a 'working draft' segmence. It e
                                                                                                                                                                                                                                                                                                                                                                                            Rowen.L. Madam.A., Olb.S., Abbasi.N., Batadatani.L., Birditt.H.,
Bloom.S., Bors.M., Dickhoff.R., Batrison.G., James.R., Lasky.S.,
Madam.A., Ratellite.A., Shaffer.L. and Bood.L.
Sequencing of human chromosome 15 D158160 p188115 region
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Homo Sapiens chromosome 15 clone BACS 194N7 and 384G18 map 15q24.
*** SEUTENCING IN PROGRESS ***, 98 unordered preces.
                                                                                Submitted (25 SEP-1999) Multimedabase Sequencing Center, University
                                                                                                                                                                                                             Kowen,L., Madan,A., Oin,S., Abbasi,N., Bar
Bloom,S., Dors,M., Dickhoff,K., Harrison,G
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JOHN (12829...1266), 14023....1835, 1472....14682, 14791....1488
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                                                                                                                                                                                                                                                               Abbasi, N., Baradarani, L.,
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	* 24125 25153; contig of 1029 app of unknown	gap of un	odlod. gap of un	* 220-5 23296: contig of 1262						* 16949 17661; contignet 713.	16948: contiq dap of	15966: contig	15418: contig		* 13092 13788: contig of 697 k	contiq	12247: contid	11447: contig gap of	10439: contig	9727: contiq qap of								. — .	2 5	_ 		contiq	dab of	* be preserved. * Description of 658 bp.	* This record will be updated with * as soon as it is available and t	* runs of N. but the exact sizes of the gaps are unknown.
of 837 bp in length unknown length	wn length	lengt!	length	An length 62 bp in length		C.	C.	- 3		of 713 bg in length unknown length	of 982 bp in length unknown length	of 548 bp in length unknown length	of 816 bp in length unknown length	of 814 bp in length unknown length	of 697 bp in length unknown length	of 844 bp in length unknown length	of 800 bp in length unknown length	or 1008 bp in length unknown length	of 712 bp in length unknown length	a of 619 bp in length Cunknown length	of 1119 bp in length unknown length	of 616 bp in length	on 626 beingth	unknown length of 471 by in length	of 930 bp in Length	of 645 bp in length						7 bp in length vn length	lengt	a be in length	n the finished sequence the accession number will	igs are represented as of the gaps are unknown.
* 53207	* 51874	* 50576	* 59261	* * 58303	* 57312	***	* * * · · · · · · · · · · · · · · · · ·	* *	* 53994	* * 53152	* 51983	* 50703	* 49438	* 47851	* 46763	* 4547U	* 43893	* 43046	* 41352	* 40020	* * * 5 1 1 1 1 1 1 1 1 1	* * 38610	* * * * * * * * * * * * * * * * * * *	** * 35273	* * 34504	* * 34747	* * * * * * * * * * * * * * * * * * *	* * 32124	* * * * * * * * * * * * * * * * * * * *	* * * * * * * * * * * * * * * * * * * *	* *	* 29923	* 2917 <i>s</i>	* 28490 *	* 27764	* 26856

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contig of 1817 bp in length
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contig of 975 bp in length
DB 36; Length 115387;
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Query Match Rest Local Similarity Matches 85: Conserv Conservative 5.1.8; 51.28; 2 Score 36.42 D 3 Prod. No. 19; 0: Mismatches 81; Indels O; Gaps 0;

QY 431 approclamataacqtoctacqeeqtoageacaateccaaqqtoadacqadaaqtoct 490 | 1.111 | 1.111 | 1.111 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.1

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Fost processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: pir2:*
4: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score atteater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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N .	Score	Mat ch	Match Length	BCI	ID	Description
_ ;	2147	100.0	168	2	875649	renin-bindind
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25	87	4.1	348	2	H75409	glycosyl hyrolase,
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beta glucosidase h	D69785	2	465	ي. پ	84	41
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fibroblast growth	S41050	2	748	بد چ	84.5	ي ي
ribosomal protein	D72093	N	580	٠. د	84.5	₩ 8
ribosomal protein	A81710	N	536	٠ ٤	84.5	37
70K antigen - Chla	A32246	N	180	3.4	84.5	36
CWH41 protein - ye	862136	Ν	× 1	4.0	3 17	نین ای
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amylase A (EC <.2	ALDYAT	ь.	585	4.0	85.5	0.8

ALIGNMENTS

RESULT S75649

remin-binding protein-related protein - Symechocystis sp. (strain ECC 5803)
RyAlternate names: protein str1975
C.Species: Symechocystis sp.
A.Varioty: ECC 6803
C.Species: Symechocystis sp.
A.Varioty: ECC 6803
C.Date: 25-Apr-1997 #sequence_revision 25-Apr 1997 #text change 20-Jnn-2000
C.Accession: S75649
R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-146, 1996

DNA Res. 3, 109-186, 1996 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synocherys

A:Reference number: \$74322; MUID:97061201
A:Accession: \$75849
A:Accession: \$75849
A:Status: nucleic acid sequence not shown: translation not shown
A:Status: nucleic series end sequence not shown: translation not shown
A:Status: nucleic tops
A:Roleoule: type: DNA
A:Rosidnes: 1-391 - KAN A:Rosidnes: 1-391 - KAN A:Cross-references: EMHL:D90912; GR:ABOD1339; NID:g1653228; PIDN:BAA]%210.1; FID:q174
A:Note: the nucleotide sequence was submitted to the EMH Data Library, June 1996.

MIAIIRROELAOQYYQALHQDYLPFWEKYSLDRQGGGYFTCLDKKGYVFDTDKFIWLQNRQ 60 HIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
MIMIRROBLAQOYYQALHQDVLPEWEKYSLDRQGGYFTCLDRKGQVFOTDKFINLQNRQ HILLITITITITITITITITITITITITITITITITITIT
MIAHEROBLAQOYYQALHQDYLPEWEKYSLDKQGGGYFTCLDKKGQVEGTDKFTKLQNKQ
MIAHRROBLAQOYYQALHQDVLPEWEKYSLDRGGGYFTCLDRKGQVFDTDKFINLQNRQ
MIAHRROELAQQYYQALHQDVLPFWEKYSLDRQGGYFTCLDRKGQVF97DKFTKIQNRQ HITHITHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
MIAHEROBLAOOYYOALHODYLPEWEKYSLDROGGGYFTCLDKKGVEFYTOKETNLONKO HILLITTHITHITHITHITHITHITHITHITHITHITHITHITH
#I.AHRROBIJAQQYYQALHQDYLDEWEKYSLDRQGGGYFTCLDRKGQVEDTDKFINIQNRQ
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MIAHRROBLAGGYYGALHIGDYLPFWEKYSLDKGGGGYFTCLDKKGGVFFTDKFTNLGNRG
MIAHRROELANOYYOALHODYLDFWEKYSLDROGGGYFTCLDRKGVPFJTDKFIMI,QNRQ HILLITITITITITITITITITITITITITITITITITIT
1 MIAHRROELAQQYYQALHQDYLPEWEKYSLDRQGGGYFTCLDKKGQYFUTDKFIWLQNRQ 60

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A: Fitte: Molecular cloning and sequence analysis of a cDNA encoding a pol-
A: Reference number: A 85/41; MHD: 90216621
A: Reverses on: A 65/41
A: Status: preliminary
A: Status: preliminary
A: Residence: 1 402 × 100 ×
A: Cross references: GR:J05/89; NID:q164640; PIDN:AAA/HI16.1; PID:q164641
A: Cross references: GR:J05/89; NID:q164640; PIDN:AAA/HI16.1; PID:q164641
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C:Species: Sus scrota domestica (domestic pig)
C:Date: 05 oct 1990 #seephence_revision 05-bet 1990 #text_change 05-Nov
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C:Species: Rathus norvegious (Norway rat)
C:Date: 41 Mar 1992 #sequence_revision 41-Mar-1992 #text_change 20
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A: Accession: JX0187
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J. Riol, Chem. 255, 6556-6561, 1990
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   F: 185 206/Redion:
                                 F:164 189/Region: hydrophobic
                                                             C: Keywords: leucine zipper
                                                                                  "; Comment: Remin binding protein is
                                                                                     A:Cross references: GB:D1023: GB:D01086: NID:q220896; PIDN:BAA01083.1; PID:q220897
C:Comment: Benin binding protein is a protein that binds to renin to form a high molecu
                                                                                                                                                                                                                                                                       A: Fit be: Genetic and molecular properties of human
                                                                                                                                                                                                                                                                                               Rithone, H.: Takahashi, S.: Fukni, K.: Miyake, Y.
J. Biochem. 110, 494-500, 1991
                                                                                                                                                                                                                                                                                                                                                          C:Accession: JX018/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WOFAVEYNRIE - PKROWILETARHGADELAKHOR - DODONWYFALDQESKRIRQDYNVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMITICITAEOTIGEEDEETVORKAVOLUHM
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beneine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Mismatches [53; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWILEPTIVERVIACIVEEVMIDELDPETGLMREA 221
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                                                                                                                       Matches 138;
                                                                                                                                               Guery Match GO.ON: Score 645: 18-2: Length 417: Best Local Similarity 34.7%: Fred. No. 1.4e 47;
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A:Introns: 46/2; 61/4; 87/1; 144/3; 219/3; 247/1; 405/3; 449/4; 479/1
c/Keywords: leuchic zipper
E:164-189/Region: hydrophobic
E:185-206/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aptross-reterences: GH:D10242; GH:D01085; NID:q220052; PIEN:BAA01082.1; FIE:q220053 
R:Platzer, M.; Baner, D.; Brescher, B.
submitted to the EMBL Data Library, March 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Accession: JX018B; G02510
R:Inone, H.; Takabashi, S.; Fukui, K.; Miyake, Y.
J. Biochem. 110, 493-500, 1991
A:Rittle: Genetic and molecular properties of human and rat renia binding profesus with A:Reference number: JX0187; MUID:92138649
A:Accession: JX018B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Hemo sapious (man)
C:Date: 41 Mar 1992 #sequence_revision 31 Mar 1992 #text change 20 Jun 2000
                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1:417 - PLA -
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: H01368
A;Accession: G02510
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A: Residues: 1:417 · INO ·
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                                                                                                                                                                     A;Gene: RbP
                                                                                                                                                                                                          C; Genetics
                                                                                                                                                                                                                                           C:Comment: Renin binding protein is a protein that binds to renin to form a high
                                                                                                                                                                                                                                                                                         A;Ctoss-reterences: EMBL:U52112; NID:g1302657; PIDN:AAC51750.1; PID:q1302662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 HOFRDPEYGEWFGYINQEGKVALTIKGGPFKGCFHVPRCLAMGEGTI. 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 AVTPTGEFVDSFEGREENPGHGTEAMWEMMDTAQRSGDRQEQAT AVVENTEEYAWDE 27s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE SDYFAAMAESOYALASGAODAKATALQAYNNVLR ROHNDKGQYDKSYDDERDLKSLAVD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 SHEADREYGEWEGYLNRKGEVLLNLKGGKWKGGFHVPKALWLCAETL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 RROELAQQYYQALHQD-1-VLPFWEKYSLDRQGGGYFTr'LDRKGQVFDITKFIWLQNRQV-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVSEDGKELFGCLGRHONFGHTLEAGWFLLOYALRKGDFKLORHTLDKFLLLFFHSGWDF 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WQEAVEYNKLE: PKPQWLEIARHGADELARHGK DQDONWYEALDQEGKPLRQPYNVE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VEOLGEED- EEMIDKY-AELGDWCAHRILQHVOKDGGVVLE 227
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5 RROELAQQYYQALHQD-- VLPFWEKYSLDRQGGGYFTCLDRKGQVFDfDKFTWLQNROV 61

75; Mismatches 163;

s opul

Conservative

3 KEKETLQAWKERVGGELDRVVAFWMEHSHDODHGGFFTFGGAREGRVYFDLKYVWLGGRQV 52

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A:Cross-references: EMHL:L19201; NID:q304961; FIDN:AAH03013.1; PID:q304984
A:Note: the uncleatide sequence was submitted to the EMBL Data Library, October 1993
R:Blattner, F.R.; Plunket III, 6:; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd.
A.: Rose, D.J.; Man H.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical 48K protein (glnA-fdhE region) - Escherichia coli
W.Alternate namos: hypothetical protein t418
C.Species: Escherichia coli
C.Date: 19-May-1994 #Sequence_revision 01-Sep-1995 #text_change 04-Mar-2000
C.Accession: S40824; 755193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 277, 1453-11-1, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: Ab4720; MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Reterence number: $40802; MOID:93347969
A:Accession: $40824
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
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Nucleic Acids Res. 21, 3391-3398, 1993
A:Hitle: Analysis of the Escherichia coll genome. III. DNA sequence of the region
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G:Superlamily: Escherichia coli hypothetical 48K protein (glnA-idhE region)
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A:Experimental source: strain K-12, substrain MG1655
Colemetics
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Best Local S
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144 IEIIEKYFWSEEEQMCLESWDEAFSKTEEYRG-----GNANMHAVEAFLIVYDVTHDK 196
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                                                                                                                                                                                                                                                                                                                                                                                                           y Match 6.9%; Score 148; DB 2; Length 418; Local Similarity 21.1%; Pred. No. 5.5e-05;
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                                                                                                                                                                                                                                                        38 FGWIXINKGOTKEEMGTHLWITAKMLHVYSVA------AAMGRPGAYSLVDHGTKAM 87
                                                                                                                                                                                                                                                                                            *8 FILTLDRKOOV EDIDKEIWI.QNRQVWQFAVFYNRI.EFKPQWI.EIARHGADEI.ARHG---- 92
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                                                                                                                            NGALKDKKYGGWYAGVNDEGVVDASKOGYOHF---FALLGAAS-AVTIGHPEAKKILDYI 143
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                                                                                                                                                                                          ----RDQD GNWYFALLQEG--KPLRQPYNVFSDCFAAMAFSQYALASGAQEAKAI---- 141
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                                                              ---ALQAYNNVLRRQHNPKGQYEKSYPGTRPLKSLAVIMILANUTLEM 186
                                                                                                                                                                                                                                                                                                                                                                             Mismatches 186; Indels 78;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                             17;
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EVILNLKGG 367 	ANG I P
EILVALAKGHQAIGUEKCWQWFEKVHDYAWSHF 34.2 	QY 294 HPP-QQLEW-DQKLWWVHLETLVALAKGHQATGQE
NPGHGIEAMWEMMOJAQRSGDRQLQEQAJAVVLNTLEYAWDEEEFGGIFYFLDRQG-292 	Qy 238 NPGHGIEAMWEMMGIAQRSGDRQLQE
OTVREVMIDELDDEIGIMREAVIPIGEEVDSFEGRIJ, 237 	Oy 195 VEEVLA
-PKGOYEKSYPGIRELKSLAVPMILANGILEMEWILFEII 194 	Oy 156 -PROGYEKSYPGIRPLKSLA 1
PY-NVESDCEAAM-AESQ-YALASBAQEAKATALQAYNNVLKRQHN	Qy 113 PY-NVESDCEAAM-AESQ-YALASGAGEA :
NROVWOFAVEYNRLEPKYOWLETARHGADELARHGRDODGNWYFALDGEGKPLKO 112 	Oy 58 NROVWOFAVEYNRLEPKTOWLETARHGADELARHGRDODGN : : : : : :
1%; Score 108.5; DH 2; Length 607; 7%; Pred. No. 0.22; 47; Mismatches 127; Indels 129; Gaps 25;	Query Match 5.1%, Score Best Local Similarity 22.7%; Pred. Matches 89; Conservative 47; Mi
Reference number: S74322; MUID:97061201 Accession: S77092 Status: nucleic acid sequence not shown; translation not shown Status: nucleic acid sequence not shown; translation not shown Molecule type: DNA Molecule type: DNA Residues: 1-607 -KAN> Cross references: EMBL:D90008; GB:AB001339; NID:q1652725; PIDN:BAA17650.1; 177 (165 Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1936 Superfamily: Synechocystis hypothetical protein slr1855	24 24 24 24 24 24 24 24 24 24
<pre>i, H.: Tanaka, A.: Asamizu, E.: Nakamura, Y.: Miyajima: Lakeuchi, C.: Wada, L.: Watanabe, A.: Yamada, M.: Yus the genome of the unicellular cyanobacterium Syn. 's-cys</pre>	R:Kaneko, T.: Sato, S.: Kotani, H.: Tan o, K.: okumura, S.: Shimpo, S.: lakeuch DNA Res. 3, 109-136, 1996 Arfitle: Sequence analysis of the genom
- Synechocystis sp. (strain PCC 6864) _revision 25-Apr-1997 #text_change zō Jun 2000	RESULL 6 877092 Synothetical protein stil855 - Synechocystis sp. (strain PC CiSpecies: Synechocystis sp. A:Varioty: PC 6803 A:Varioty: PC 6803 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_ch. C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_ch.
GCEHVPR 377 III HILHOLVIDR 397	QY 354 LINKRGEVLLNIKGGKWK+ - GCEHVPR : : : : DD 359 LIJADNKVTTKVWDGKODIYHLLHCLVIPR
PPOOLEMBOKLWWPH: FILVALAKGHOAIGGEKGWOWEEKVHDYAWSHFADDEYGFWFGY 354 FRYRWFIVEAAMGTAYALYTVTGDRQYEIWYGTWWEYGIKYLMGYENGSWWGE 348 PVVRERVRWFIVEAAMGTAYALYTVTGDRQYEIWYGTWWEYGIKYLMGYENGSWWGE 348 FRYRWFIVEAAMGTAYALYTVTGDRQYEIWYGTWWEYGIKYLMGYENGSWWGE 348	OF 54 PROGLEMBOKLWWAREFILVALAKGHOAL
HRIEAMWENNDIAQREGIE QUQEQALAVVLNTLEYAW-DEEFGGIFYFLDRQGH 274 (QY 241 HGTEAMWENNDTAQKSGDR
EWLLPPTTVEEVLAQTVREVMIDELDPEIGLMREAVIPTGEFVUSSEGRILNPG 240 :II	QY 187 EWLLPPTTVEEVLAQTVREVMTDEL Db 197 KWIDHAIRVASVITHDVAKNNHYKVNEHE

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DNA Ros. 1, 1-14, 1994
A: Fitte: Systematic sequencing of the 180 kilobase region of
A: Reference number: S65967; MUID:96051385
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A:Rectedence number: $55887
A:Rectedence S55887
A:Accessor on $55887
A:Molecule type: mRNA
C:Superlamily: homocyanin
                                                                                                                                                                                                                                                                                                    A:Status: preliminary: nucleic acid sequence not shown: translation not shown \Lambda; M \text{-} Leonle \ \text{type: DNA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cibite: 28 oct 1996 #sequence_revision 13 Mar 1997 #text_change 20 Jun
CiArcession: $66006; $66003; C70085
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C:Date: 15 Dul 1999 #sequence, revision to Nov 1995 #text change to May-2000
                                                                                                                                                                                                                                                    A: Cross references: EMBL:D26185; NID:q467326; PIDN:BAA05212.1; PID:q467366
                                                                                                                                                                                                                                                                                A: Restrictions: 1 689 - GIA
                                                                                                                                                                                                                                                                                                                                                      A: Accession: S66006
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PISSTASTILAÖAUHAÖAUHUDAGHAOMIKAMININGATAMINDAGHAOMIKATI

1 MIAHRROEL----AQQYYQALHQDVLJEWEKYSLDRQGGGYFTGLLJKKGQVFDJDKFIW 55

51; Mismatches 155;

Indots 12%;

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A.: Ebrilich, S.D.: Emmerson, P.T.: Ebrian, K.D.: Errindton, J., Fabret, C.: Perrar, Nature 400, 249-256, 1997

A:Authors: Foulage, D.: Fritz, C.: Fojita, M.: Fujita, Y.: Fuma, S.: Galizzi, A.: Galicch, J.: Harwood, C.K.: Henart, A.: Hilbert, H.: Holsappel, S.: Hosono, S.: Hullo, M. Koetter, P.: Konlostein, G.: Krodi, S.: Kumano, M.: Kurita, K.: Lapidus, A.: Lardino A:Authors: Lauber, J.: Lazarevic, V.: Lee, S.M.: Levime, A.: Liu, H.: Masuda, S.: Man y. M.: Oudawa, K.: Oujwara, A.: Oudeqa, B.: Park, S.M.: Levime, A.: Liu, H.: Masuda, S.: Man y. M.: Oudawa, K.: Oujwara, A.: Oudeqa, B.: Park, S.M.: Lavido, Y.: Sato, I.: Scanl A:Authors: Schicith, S.: Schiceter, R.: Scottone, F.: Scklapchi, J.: Sckowska, A.: Scakouchi, M.: Hamakoshi, A.: Ianaka, Y.: Frepstra, P.: Ioduoni, A.: Iosato, V.: Hebiya, T.: Winters, P.: Wipat, A.: Yamsnoto, H.: Yasumoto, K.: Yata, K.: Yoshida, A.: Mithors: Yoshikawa, H.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Iuthors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
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A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.F.: Zumsrein, E.: Yoshikawa, H.: Darchi, A.
A:Authors: Yoshikawa, H.: Yoshikawa, H.: Darchi, M.: Yoshik
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C:Species: Felis silvestris catus (domestic cat)
C:Date: 26-Nov 1999 #sequence_revision 26 Nov 1999 #text_change 26-Nov 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A: Fitte: Purification of teline Tysosomal alpha-mannosidase, A:Reference number: Z22083; MUID:98060744 A:Accession: I42219
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A:Experimental source: Strain 168
C:Genetics:
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Query Match 4.5%; Score 97.5; DB 3; Best Local Similarity 18.5%; Fred. No. 3.9; Matches 75; Conservative 51; Mismatches 155;
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Db 257 VADEHVDPEFGTGAVKVIPAHD-PNDFEIGVRHQLPMPSILDTK 299 UV 244 GKLLNPGHGIEAMWEMMDIAQRSGDRQLQEQAIAVVLNTLEYAWDEEFGGIEYFLDRQGH 293	
NPKGQYEKSYPGTRPLKS	
74 KPQWLEIARHGADELAKHGRDQDGNWYEALDQDGKPLRQPYNVESDGEAAMAESQY 	
OF 25 WEKYSIDROAGGYFICIDRKGQVFDIDKFIWION	
Guery March 4.4%; Score 95; DB 2; Length 876; Best Local Similarity 19.8%; Pred. No. 5.3; Matches 74; Conservative 47; Mismatches 131; Indels 122; Gaps 18;	
A:Experimental source: strain H37kv C;Genetics: A:Gene: vals C;Supertamily: valinetRNA ligase	
ry: nucleic acid sequence not shown: translation not shown:	
A:Authors: Spires. R.: Sulston, J.E.; Taylor, K.: Whitehead, S.; Barrell, B.G. A:Hitle: Deciphoring the biology of Mycobacterium tuberculosis from the complete genome A:Reletence number: A70500: MUID:98295987 A:Accession: 470864	
Ricole, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A. Rowerts, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature, 364, 537-544, long	
RESHIL 10 G70864 probable valS protëin : Mycobacterium tuberculosis (strain H37RV) C1Species: Mycobacterium tuberculosis C1Date: 17-101-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C1Dacessin: (J7-M56)	
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415 TMCSDEQVE NANMMERCHIDELIDELIDELIDE	
OY 268 VVI.NIT.EYAWDEEFGGTFYFI.DROGHFPOOLEWDQKI.WWVHI.ETI.VALAKG-HQATGQF- 325	
CY 208 IDFLIDETGLIKEAVIPIGEFVDSFEGRILINISHGIEAMWEMMDIAQRSGDROLQEQAIA 267	
QY 153 QHNPKGQYEKSYPGTRPLKSLAVPMILANLTI.EMEW LLPPTTVEEVLAQTVREVM 207 :	
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120 VE:IAFESRWHIQOTNATQEVVKDLVRQGRLETANGGWVNNUEA	
OF S6 LONGOVWOFAVEYNKLEPKPOWLETAKHGADELAKHGKDO: DGNWYF 101	

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                                                                                                                                                                                      adenylate cyclase (EY 4.6.1.1) uacl + smut fungus (Ustilado maydis)
C:Species: Ustilado maydis (corn smut)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09 Sep-1997
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hypothetical protein FTRA7.10 - Cachorhabditis elemans
C:Species: Caenorhabditis elemans
C:Date: 15-oct-1999 #sequence_revision 15-oct-1999 #fext change 15 oct 1999
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                                                    R:Gold, S.: Duncan, G.: Barrett, K.: Kronstad, J. Genes Dev. 8, 2805-2816, 1994
A:Tille: CAMP regulaties morphogenesis in the fundal pathogen Ustilado maydis A:Reference number: A55481: MUID:95087882
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A):Reference number; 219327
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A;Accession: A55481
A;Status: proliminary
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A; Introns: 27/1; 182/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:294377: PIDN:CAB07572.1; GSPBB:GN00023; PESF:F13A7.10
A;Experimental source: clone F13A7
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A:Molecule type: DNA
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A;Molecule type: DNA A;Residues: I 2493 -GDL> A;Cross-references: GB:L43918; NID:q603939; FID:q603940 A;Note: nucleotide sequence not given; amino acid sequence not complete C;Genetics:

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Ent. J. Riochem. 178, 403-412, 1988
A; fittle: Esmollins interruptus bemoryanin. The amino acid sequence of subunit b and and
A; Reference number: 802707; MUID:89091175
A; Accession: 802707
A; Motocule type: protein
                                                                                                                                                                                                               As Contents: annotations: X ray crystallography, 3.2 and stroms. As Note: the crystals contained a mixture of a and b chains; the structure was fit to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N:Alternate names: hemocyanin 90K chain
C;Species: Panulirus interruptus (California spiny lobster)
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C:Supertamily; yeast adenylate cyclase catalytic domain homology; lencine rich
  F193 98,483 502,562 609/Disullide bonds:
                        E:176 398/Domain: 2, earboxyl terminal (Dos)
                                                                                                                                    CoSupertainily: house
                                                                                                                                                          C:Comment: This hemoeyanin is a hexamer of a number of different chains, of which a,
                                                                                                                                                                                                                                                                         A: Reference number
                                                                                                                                                                                                                                                                                                    A: Title: Crystal
                                                                                                                                                                                                                                                                                                                        R:Volteda, A.: Bol, W.G.J.
J. Mol. Hiol. 209. 19 2/9, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                              Addition 3.2 and strong structure of the copper containing oxygen-carrying protein Panul
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 309, 23-29, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Note: 32 Glu. 49 Glu. 122 Gly. 130-Lys. R:Gaykema, W.P.J.: Hal. W.G.J.: Vereljken.
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A; Note:
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(1157 | 1180/bomain: leneine rich alpha 2 glycoprotein repeat)
(1151 | 203/bomain: leneine rich alpha 2 glycoprotein repeat)
(1227 | 1240/bomain: leneine rich alpha 2 glycoprotein repeat)
(1237 | 1240/bomain: leneine rich alpha 2 glycoprotein repeat)
(1250 | 1242/bomain: leneine rich alpha 2 glycoprotein repeat)
(1316 | 1482/bomain: leneine rich alpha 2 glycoprotein repeat)
(1318 | 1404/bomain: leneine rich alpha 2 glycoprotein repeat)
(1409 | 1411/bomain: leneine rich alpha 2 glycoprotein repeat)
(1518 | 1518/bomain: leneine rich alpha 2 glycoprotein repeat)
(1518 | 1518/bomain: leneine rich alpha 2 glycoprotein repeat)
                                                                  :Keywords: coppet: algeoprotein; hemolymph: oxygen carrier
:1 [75]bomain: 1, ameno terminal about.
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Best Local Similarity 22.6%;
Matches 55; Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                            annotation: X ray crystallography, 3.2 angstroms
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Vereljken, J.M.; Soeter, N.M.;
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Bak, H.J.; Beintema,
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R:Ferreira, L.M.A.: Harlewhod, G.P.; Barker, F.J.; Gilbort, H.J.
Submitted to the EMBL Data Library, Ampust 1991
A:Description: The collodextrindse from pseudomonas fluorescence
A:Reference number: S16849
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A:Residues: 1-262, C',264-291, K',293-748 <PE2>
A:Cross-relerences: EMML:X61299; NID:q45501; PID:q45502
C:Genetics:
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A;Status: preliminary
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A; Accession: $19652
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Biochem. J. 279, 794-799, 1991
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C:Date: 13 Jan-1995 #Secure _revision 13-Jan-1995 #fext change 15-est
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                                                    130 ALASGAQEAKATALQAYNNVLRRQHNPKGQYEKSYPGTRPLKSLAVPMILANL
455 SCSATNNPSSVTRIHAYDK --
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18.4%; Prod. No. 7;
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THE SOLE EPYDYTWAEWKGMVEEAY-QAINEVNPHNKLIIVEĞISANANİQDĞIPDISVPVPRGSIDL 561 CY 283	265 AIAVVI.N -TLEYAWDEEEG	347 YGEWEGYLNREGEVLLNIKG 366 :	RESULT 15 H75139 IsoloucyI-tBNA synthemase (iles) PABU515 - Pyrococcus abyssi (strain Orsay) Coshucies: Pyrococcus abyssi Coshuce: Eyrococcus abyssi Coshuce: 20-Aun-1999 #sequence_revision 20-Aun-1999 #text_change 20-Jun-2000 Coshuce: 20-Aun-1999 #sequence_revision 20-Aun-1999 #text_change 20-Jun-2000	onery Match Rest Local Similarity 20.4%; Pred. No. 18; Matches 56; Conservative 24; Mismatches 47; Indels 148; Gaps 14;	OY 153 CHNPKGQY	QY 185	OY 231 SEEGRELINEGHOLEAMWEMMDIAORSGDROLOEGALAVVI.NILEYAWDEEFGGIFVELDR 290	CY 291 ORTHPOOLEWINGKLIMMVHLELLIVALAKGHQATGQEKÇMOMPEKVHIYAMISHFA 343 H;	QY 344 DPEYGEWINY LNRRGEVILLNEKGGKWKGGE 474	Qy 265 ALAVVIN: TLEY Qy 265 ALAVVIN: TLEY 11: 1 Db 622 G-RIVINPIVIEQ Qy 688 HEELVALAKGHO Db 674
622 G-KIVINPIVLEQUMEEHFGYLRELGYGILIGEEGGNMDWPGAKSSQADKNAW	17 YGEWEGYLNERGEVLINLEG 466 : : : : : : : : : : : : : : : : : :	15 yl-tRNA synthetase (iles) PABO515 - Pyrocoecus abyssi (strain Or yr-tRNA synthetase (iles) PABO515 - Pyrocoecus abyssi (strain Or 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun- sion: H75189		A:Molecule type: DNA A:Residues: 1-1067 KAM's A:Pross-references: GH:AJ248285; GH:AL096836; NID:g5458067; PIDN:CAB49833.1; PID:g5458 A:Experimental source: strain Orsay C:Genetics: A:Gene: lles: FAB0615 C:Superlamily: IsoleucinetRNA ligase	tle type: finA los: 1-1067 -KAM> references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49833.1; PID:g54 mental source: strain Orsay lles; PABGEL illes; PABGEL amily: isole-ucinetRNA ligase amily: isole-ucinetRNA ligase Match 4.3%; Score 92; DB 2; Length 1067; socal similarity 20.4%; Pred. No. 13; socal similarity 20.4%; Pred. No. 13;	Le type: INA Locs: 1-1067 -KAM> references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49833.1; PID:g54 mental source: strain Orsay lles; FAB6615 lles; FAB6615 A.38: Score 92; DB 2; Length 1067; Local similarity 20.4%; Pred. No. 14; Local similarity 20.4%; Pred. No. 14; S6 OHNPKGUY	Le type: DNA Les: FINDAT - KAMP* ROS: FINDATA - ROS: FINDATURE -	Le type: DNA Less: DNA7 - KAMPs Less: DNA7 - KAMPs Treferences: GH:AJ248285; CH:AL096836; NID:g5458067; PIDN:CAH49833.1; PID:g54 mental source: strain orsay cs: Less: PABOLD amily: Isol-prime: TENA Lidase Match 4.3%: Score 92; DR 2; Length 1057; Match 56: Conservative 24; Mismatches 47; Indels 148; Gaps 14; ss 56: Conservative 47; Mismatches 47; Indels 148; Gaps 14; ss 56: Conservative 47; Mismatches 47; Indels 148; Gaps 14; ss 56: Conservative 47; Mismatches 47; Indels 148; Gaps 14; ss 56: Conservative 47; Mismatches 47; Indels 148; Gaps 14; ss 56: Conservati	Le type: DNA Les type: DNA Les train orsay references: GR:AJ248285; GR:AL096836; NID:g5458067; PIDN:CAH49833.1; PID:g54 mental source: strain orsay res: lles; PABGEL; lles; PABGEL; lles; PABGEL; A.4%: Score 92; DR 2; Length 1067; Local Similarity 20.4%; Pred. No. 13; Length 1067; A.4%: Score 92; DR 2; Length 1067; Length 1067; A.4%: Score 92; DR 2; Length 1067; Length 1067; ALAW: Pred. No. 13; Length 1067; ALAW: Gaps 14; Length 1067; L	Reanonymous, Gesubmitted to the submitted to the Accession: But Ac
622 G-KIVINPIVLEQUMEEHFGYLKELGYGILIGEFGGNMDWPGAKSSQADKNAW	17 YGEWEGYLNERGEVILNING 765	g1-tRNA syntherase (iles) PAHO516 - Pyrococcus abyssi (strain Orsay) 20: Pyrococcus abyssi 20:Aua-1999 #sequence_revision 20:Aua-1999 #text_change 20:Jun-2000 sion: H75149 nous, Genoscope ed to the EMHL Data Library, July 1999 [ption: Pyrococcus abyssi genome sequence: insights into archaeal chromosome segmence number: A7500] sion: H75149 sepreliminary	pe H. Data Library, July 1999 Poecus abyssi genome sequence: insights into archaeal chromosome s A75001		4.3%; Score 52; DB 2; Length 1057; cal Similarity 20.4%; Pred. No. 13; 56; Conservative 24; Mismatches 47; Indets 148; Gaps	Justy Match Just Local Similarity 20.4%; Pred. No. 13; Matches 55; Conservative 24; Mismatches 47; Indets 148; Gaps Matches 56; Conservative 24; Mismatches 47; Indets 148; Gaps 153 OHNPROOFPKSY	JUNETY Match 4.3%: Score 92: DB 2: Length 1067: wish Local Similarity 20.4%: Pred. No. 13: Jatches 56: Conservative 24: Mismatches 47: Indels 148: Gaps 15 OHNPKGDY	A.3%: Scote 92: IBB 2: Length 1057: west Local Similarity 20.4%: Pred. No. 13: Authors 55: Conservative 24: Mismatches 47: Indets 148: Gaps 153 OHNPKOOY:	## A.3%: Scote 92: DB 2: Length 1057: ## Pred. No. 18: ## Astrines 55: Conservative 24: Mismatches 47: Indets 148: Gaps ## Attrines 55: Conservative 24: Mismatches 47: Indets 148: Gaps ## It 153 OHNERGOY:	A:Molecule type A:Mosidues: 1-1 A:Cross refered A:Experimental C:Genetics: A:Gene: 1les: E C:Superiamily:

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45.					
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